

FIG. 1A

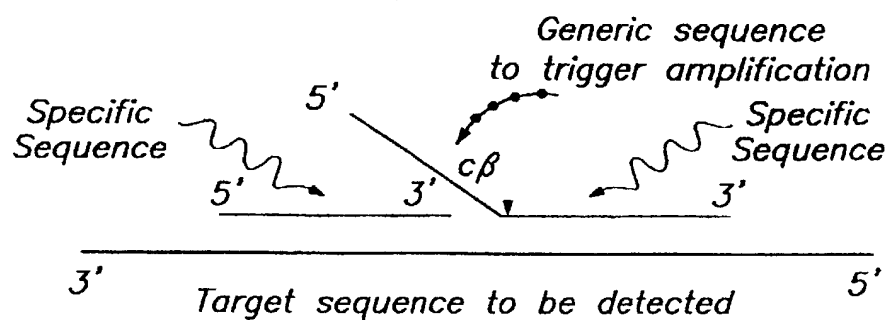


FIG. 1B PART ONE: TRIGGER REACTION

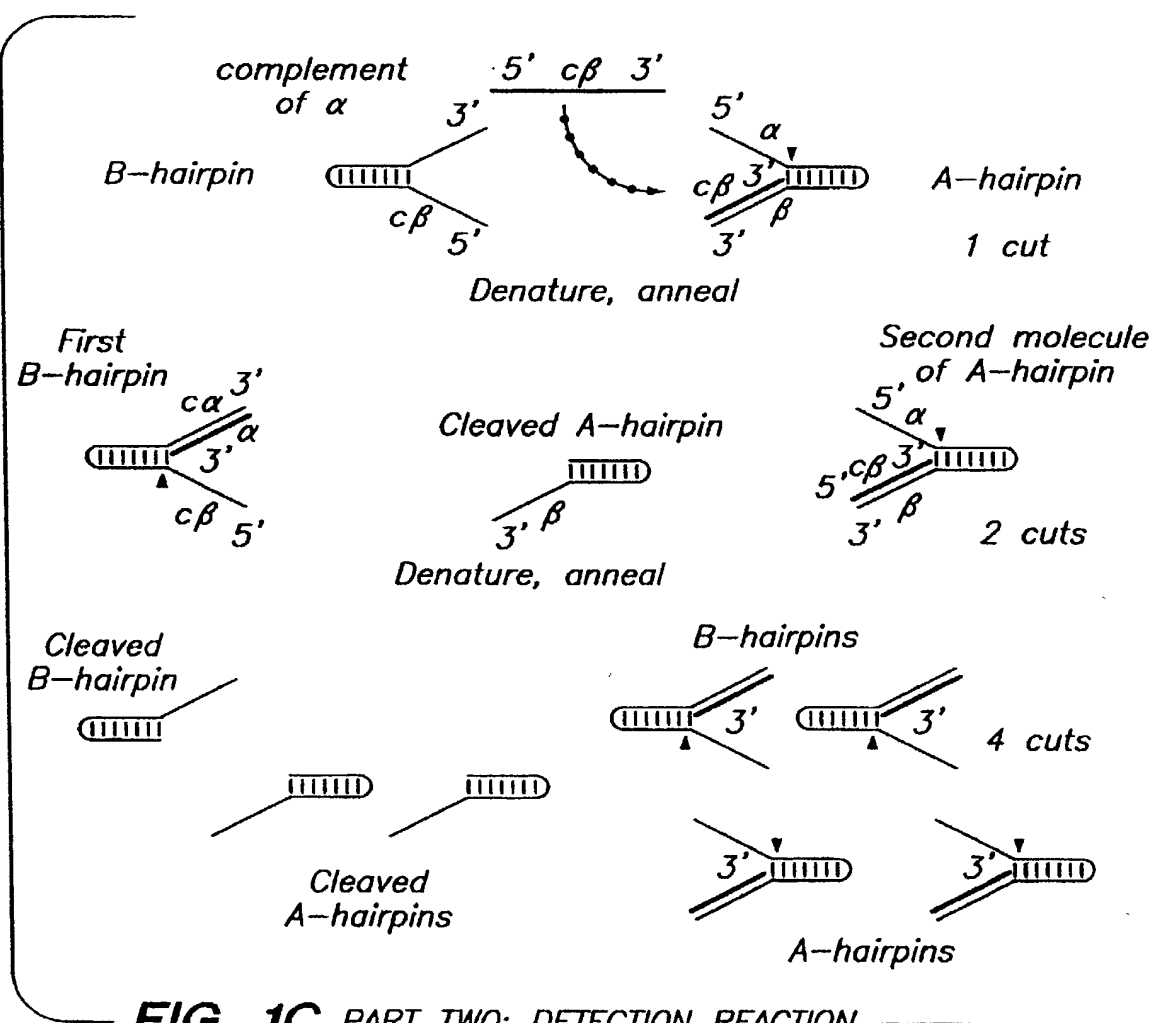


FIG. 1C PART TWO: DETECTION REACTION

$$\frac{1}{\sqrt{\pi}} \int_{-\infty}^{\infty} f(x) e^{-x^2} dx = \frac{1}{\sqrt{\pi}} \int_{-\infty}^{\infty} f(x) e^{-x^2} dx$$

DHAPTAQ [SEQ ID NO:1]	A.G. G.	G.	70
DHAPTFL [SEQ ID NO:2]	.	C. G.	67
DHAPTHH [SEQ ID NO:3]	GA.	G. A.	70

DNAPTAA	CA	6	6	140
DNAPTFL	T	6	6	137
DNAPTTH		6	6	140

DNAPTAD	C.....	A.....	207
DNAPTFL	A.....	GT.....	204
DNAPTTH	TAA.....	210

DNAPTAQ	6. 66.	6.	277
DNAPTFL			274
DNAPTTH	GA.	6.	280

DNAPIAO	A.....G.....G.....	347
DNAPIFL	G.....I.....A.G.....I.....I.....	344
DNAPIIHI.....A.G.....I.....A.G.....	350

FIG. 2B

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MAJORITY [SEQ ID NO:7]  CGAGCGGAGGAGGCTXCTGGCCACCCTGGCCAAAGAAAGCGGGAAGGGGTACGAGGTCGGCATCCTC
DNAPTAQ [SEQ ID NO:13]  .....G.....G.....C.....C.....  417
DNAPTFL [SEQ ID NO:2]  T.....G.....CG.....  414
DNAPTTH [SEQ ID NO:3]  .....T..C.....  420

MAJORITY  ACGCGGACCGCGACCTCTACGAGCTCGTTCCGACCGCATCGCGGTCCTCCACCCCGAGGGGTACCTCA
DNAPTAQ  .....AAA.....T.....GA.....  487
DNAPTFL  T.....G.....G.....A.....T.....G.....  484
DNAPTTH  .....A..G.C.....G.....CC.....  490

MAJORITY  TCACCCCGCGCTGGCTTTGGGAGAACTACGGCCCTGAGGCGCGAGCACTGGGTGGACTACCGGGCGCGCTGGC
DNAPTAQ  .....C.....A.....C..C.....CC.....A..  557
DNAPTFL  .....AC.....C.C.....  554
DNAPTTH  .....A.....C.....T..C.....C.T  560

MAJORITY  GGGGACCCCTCGGACCAACCTCCCGGGGTCAAGGGCATCGGGGAGAGACCGGCCXGAAGCTCCTCXAG
DNAPTAQ  C.....GAG.....T.....G..GAG.....T..GG..  627
DNAPTFL  .....G..T..A.....G.....A..G....A..CGC  624
DNAPTTH  .....TC.....A..  630

MAJORITY  GAGTGGGGGAGGCTGGAAACCTCCTCAAGAACCTGGACCGGGTGAAGCGCGC...CXTCGGGGAGAGAGA
DNAPTAQ  .....GC.....G.....A.....  694
DNAPTFL  .....T..C..C.....A.....T..G.....C  691
DNAPTTH  .....A.....A....A.AAA.G.....  700

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CGAGCGGAGGAGGCTXCTGGCCACCCTGGCCAAAGAAAGCGGGAAGGGGTACGAGGTCGGCATCCTC

[illegible]

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FIG. 2D

MAJORITY [SEQ ID NO:7]	CGGGGXTCTCCTCGCCGAGGAGCTGGCGTTTGGCGCTGAAGGAGGGCCTXGACCTCXTGCCCGGGGACG	
DNAPTAQ [SEQ ID NO:1]G..T.....A.....AG.....C.....A.....T..G.....CC.....C.....	1114
DNAPTFL [SEQ ID NO:2]AA.....G.....G.....G.....C.....G.....T..C...A..A.....	1111
DNAPTTH [SEQ ID NO:3]C.....C.....C.....C.....TC.....G..A.....G.....	1120
MAJORITY	ACCCCATGCTGCTCGGCTAGCTCCTGGAGCCCTCGAACACGACCCCGAGGGGCTGCCCGGGGCTACGG	
DNAPTAQG.....T.....T.....	1184
DNAPTFLG.....T.....T.....T.....	1181
DNAPTTHG.....G.....	1190
MAJORITY	GGGGGAGTGGACCGAGGAXGGGGGGGAGCGGGCGCTGCTXTGGAGAGGGCTCTTCCXGAACCTXXGGGAG	
DNAPTAQ	C.....G.....G.....GC.....T.....GGC.....GTG...G.	1254
DNAPTFLT.....A.....GG.....C..C.....A..C...AAA....	1251
DNAPTTHC..C.CCC.C.....C..G.....CAT..G.....CCTTA..	1260
MAJORITY	CGGCTTGAAGGGGAGGAGGGCTCCTTTGGCTTACGAGGAGGTGGAGAGCCGCTTCCCGGGTGGTGG	
DNAPTAQ	A..G.....A.....G.....G.....G.....GCT.....	1324
DNAPTFLA...A..A..AG.C..G.....G.....G.....GT...	1321
DNAPTTHC.....A.....C.....C.....A.....C.....	1330
MAJORITY	CCACATGGAGCCGACCGGGGTGCGGCTGGAGGTGGGCTACCTCGAGGCGCTTCCCTGGAGGTGGCGGA	
DNAPTAQG..C.....T...AG.....T..G.....C...	1394
DNAPTFLG.....C.....C.....C.....A...G	1391
DNAPTTHC.....A.....T.....T.....C.T.....	1400

CGGGGXTCTCCTCGCCGAGGAGCTGGCGTTTGGCGCTGAAGGAGGGCCTXGACCTCXTGCCCGGGGACG

[illegible]

DNAPTAQ	[SEQ ID NO:1]	GC.....CC.....	1464
DNAPTFL	[SEQ ID NO:2]	GC.....AG..G.....	1461
DNAPTTH	[SEQ ID NO:3]T.....G.....	1470

DNAPIAQ	C.	A.				G.	1834
DNAPIFL	GC.	G.	C.	G.	T.	G.	1831
DNAPTTH		TA.				T.G. G.	1840

DNAPTAD	C	C	C	1604
DNAPTFL	T	G	CCC	1601
DNAPTHH	C	A	C	1610

DNAPTAQ	G.	G.	T.	G.	A.	1674
DNAPTFL			A.	C.	G.	1671
DNAPTTH			G.	G.	C.	1680

DNAPTAQ		A	I	C.	1744
DNAPTFL	G.	C.	TC.		1741
DNAPTTH		G.			1750

FIG. 2F

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MAJORITY [SEQ ID NO:7] AGAACATCCCCGTCCGCACCCXCCTG66CCAGAGGATCCGGCCGGGGCTTCGTGGCCGAGGAGGGGTGGGT
DNAPTAQ [SEQ ID NO:1] .....G..T..G.....A.C.....G...C. 1814
DNAPTFL [SEQ ID NO:2] .....G.....T.....C.C.....A.....C.....C..... 1817
DNAPTTH [SEQ ID NO:3] .....GT.....C.....C.....T.....G...T....G 1820

MAJORITY GTTGGTGGCCCTGGACTATAGCCAGATAGAGGCTCGGGGTCTCTGGCCGAGGCTCTCGGGGAGGAGAAAGCTG
DNAPTAQ A.....T.....A.....G.....C..... 1884
DNAPTFL C.....T.....T.....T.....C..... 1881
DNAPTTH .....C.....C.....A..... 1890

MAJORITY ATCCGGGTCTCCAGAGGGGAGACATCCACAGCCGAGAGCCGAGCTGGATGTTGGCGTCCCCCGG
DNAPTAQ .....G.....GG.....G... 1954
DNAPTFL .....T.....T.....T.....C. 1951
DNAPTTH A.....A.....A..... 1960

MAJORITY AGGCGGTGGACCCCTGATCGCGCGGGCGGCAAGACCATCAACTTCGGGCTCCTCTAGGGCATGTCCGG
DNAPTAQ .....G.....G... 2024
DNAPTFL A.GG..A.....T.....G..... 2021
DNAPTTH .....GG.G.....G..... 2030

MAJORITY CCACGGGCTCTCCAGGAGGCTTGCCATCCGCTACGAGGAGGGGTGGCCCTTCATTGAGCGGCTACTCCAG
DNAPTAQ .....A.....T.....CCA.....T... 2094
DNAPTFL .....GG.....T..... 2091
DNAPTTH ...TA.G.....T.A.....A 2100

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CCGCGGTGGACCCCTGATCGCGCGGGCGGCAAGACCATCAACTTCGGGCTCCTCTAGGGCATGTCCGG

FIG. 2G

MAJORITY [SEQ ID NO:7]	AGCTTCCCAAGGTCCGCGCCTGGATTGAGAGACCCCTGGAGGAGCGGCAAGAGCGGGGTACGTGGAGA	2164
DNAPTAQ [SEQ ID NO:13]	2164
DNAPTFL [SEQ ID NO:2]A.....GG.....G.....C.CC.....T.....	2161
DNAPTTR [SEQ ID NO:3]A.....A.....G.....A.....C.....A.....	2170
MAJORITY	CGCTCTTGGCGCGCGCGGCTACGTGCCCGAGCTCAAGCGCGGCTGAAGAGCGTCCGCGGAGCGCGCGGGA	
DNAPTAQC.....A.....AG.G.....C.....	2234
DNAPTFLT.....C.....	2231
DNAPTTRAA.AA.....CA.....C.....	2240
MAJORITY	CGGCATGGCCCTTCAACATGCCCGTCCAGCGGCACCGCGCGGACCTCATGAAGCTGGCCCATGGTGAAGCTC	
DNAPTAQT.....	2304
DNAPTFLG.....CG...T	2301
DNAPTTRC.....	2310
MAJORITY	TTCGCCCGGCTXCAGGAAATCGGCGCCAGGATGCTGCTXCAGGTCACGAGGAGCTGGTCTCGAGGCGCG	
DNAPTAQA.....GG.....T.....	2374
DNAPTFLT.....C.....G.....TT.G.....G.....	2371
DNAPTTRC..C.G..G.....C.C.....C.....CC.....G.....	2380
MAJORITY	CCAAAGAGCGCGCGGAGGCGGTGGCCGCTTTGCCCAAGGAGGTCATGGAGGCGGCTCTATCCCGCTGGCCGT	
DNAPTAQA.....A.....CC.....CGGC.....G.....	2444
DNAPTFLG..C.....AG..A.....GG.....CAG..	2441
DNAPTTRC...C.....C...A.....G.....C.....AA..C.....C.....	2450

$$\frac{d}{dt} \left(\frac{\partial L}{\partial \dot{x}} \right) = \frac{\partial L}{\partial x}, \quad \frac{d}{dt} \left(\frac{\partial L}{\partial \dot{y}} \right) = \frac{\partial L}{\partial y}, \quad \frac{d}{dt} \left(\frac{\partial L}{\partial \dot{z}} \right) = \frac{\partial L}{\partial z}$$


[illegible]

1

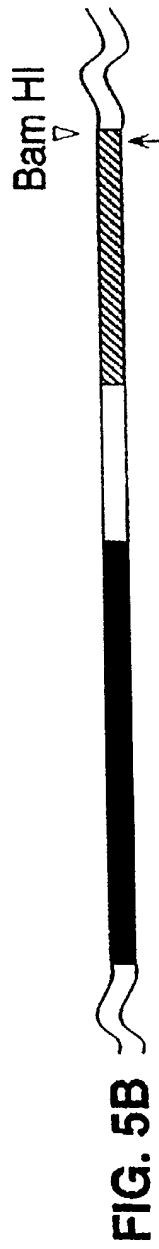
[illegible]

FIG. 3C

MAJORITY	[SEQ ID NO:8]	SFPKVRAWIEKTEEGRRRGYVETLFGRRRYVPDLNARVKSUREAAERMAFNMPVGGTAADLKKLAMVKL	
TAQ PRO	[SEQ ID NO:4]E.....	768
TFL PRO	[SEQ ID NO:5]G.....Y.....R.....	767
TTM PRO	[SEQ ID NO:6]K.....	770
MAJORITY FPRLEXMGARM LQVHDELVL EAPKXRAEXVAALAKEVMEGVYPLAVPLEVEVGXGEDWLSAKEX			
TAQ PRO	E.....E...A...R.....I.....	833
TFL PRO	O.L.....D...R.....W.O.....L.....	831
TTM PRO	R.....L.....OA...E...A...KA.....M.....G	835

400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500

(The following information was obtained from the records of the Federal Bureau of Investigation, Department of Justice.)



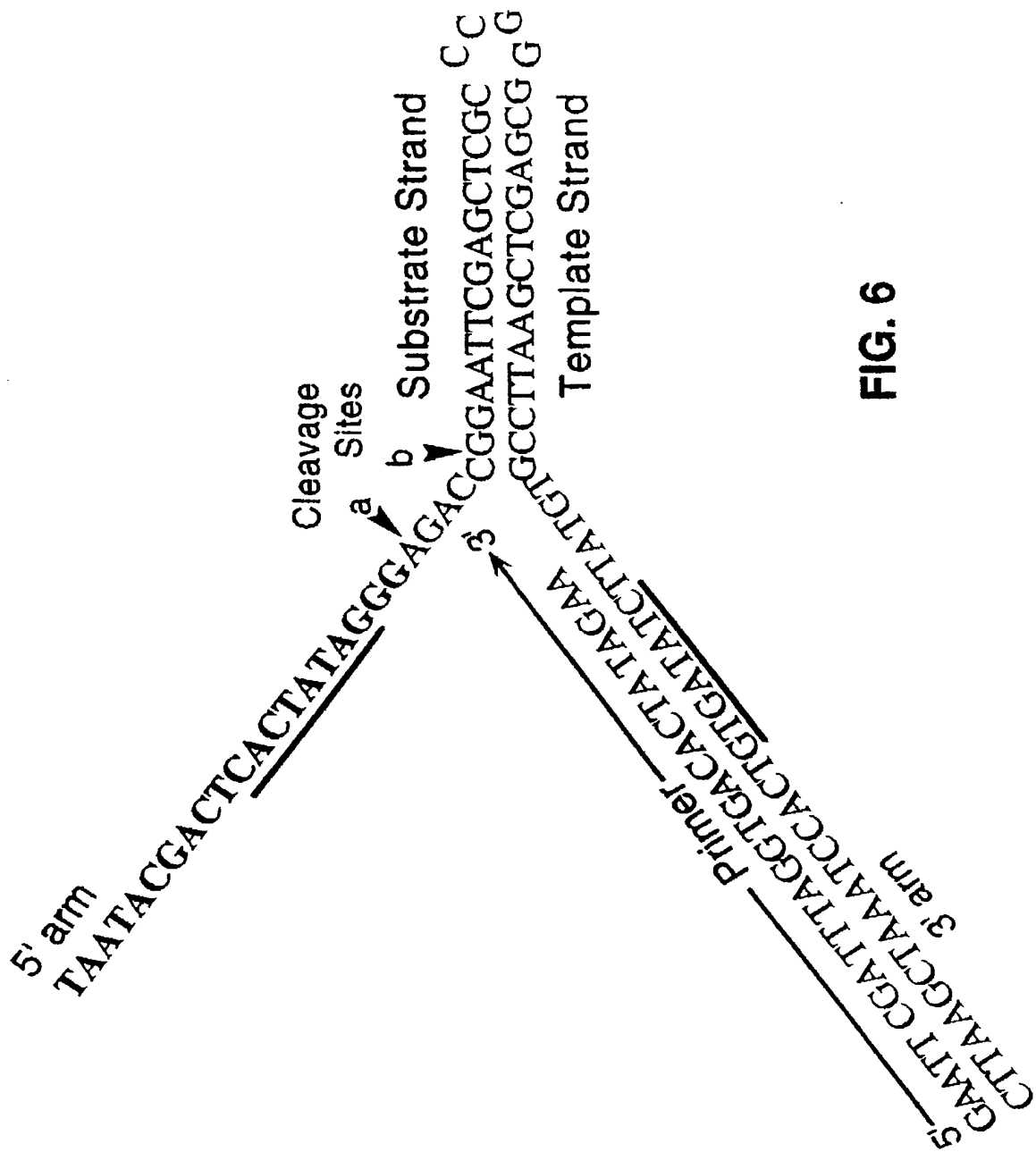


FIG. 6

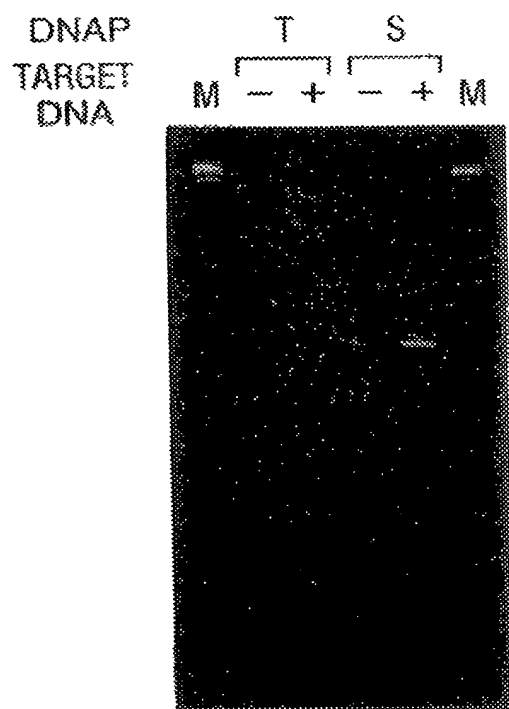


FIG. 7

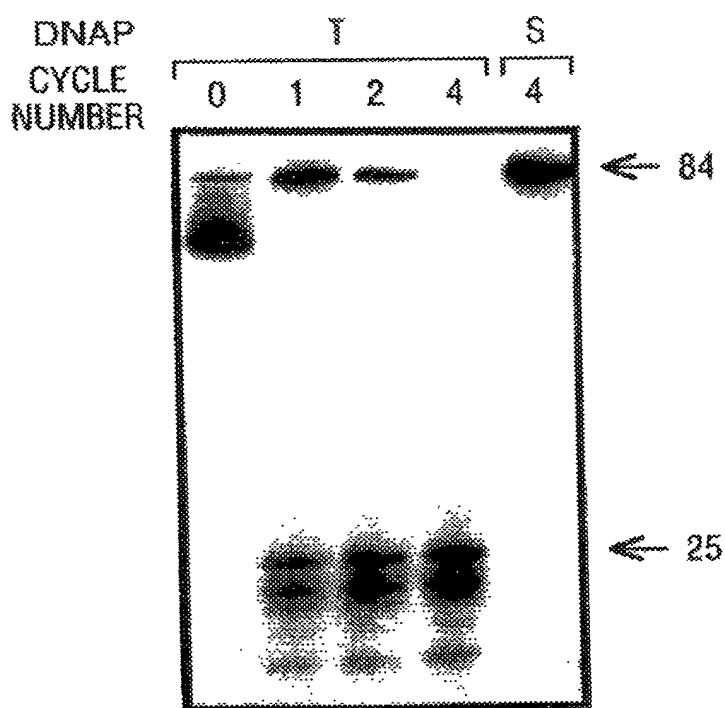


FIG. 8

	1	2	3	4	5	6
DNAP-T:	-	+	+	+	+	+
MgCl ₂ :	+	-	+	+	+	+
dNTPs:	+	-	+	-	+	-
Primers:	+	-	+	+	-	-

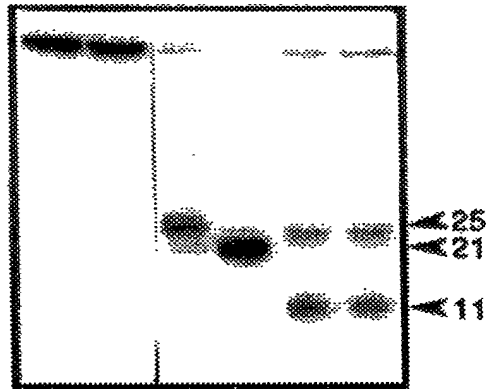


FIG. 9A

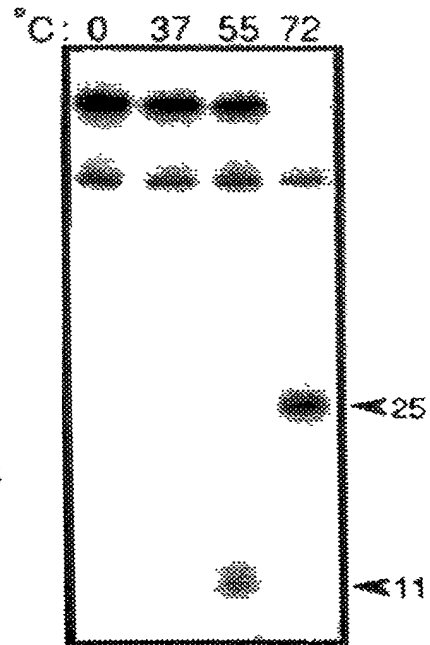


FIG. 9B

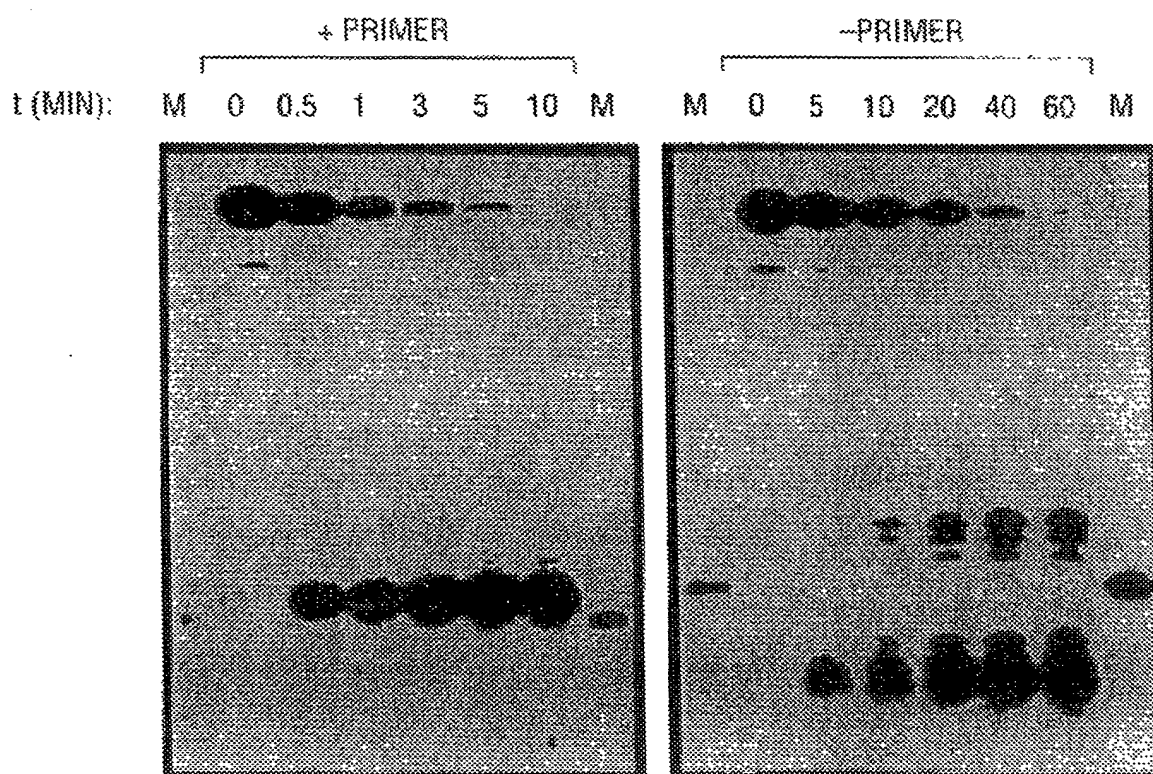


FIG. 10A

FIG. 10B

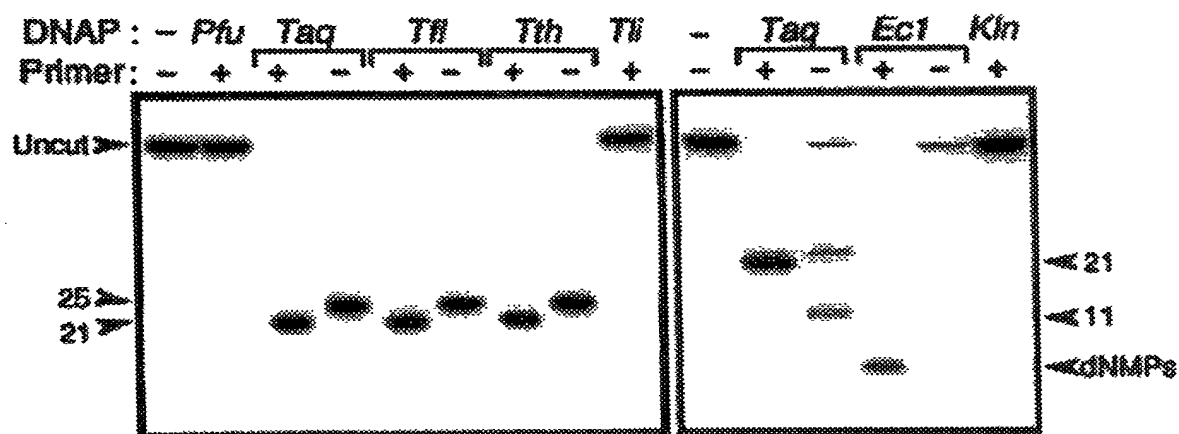
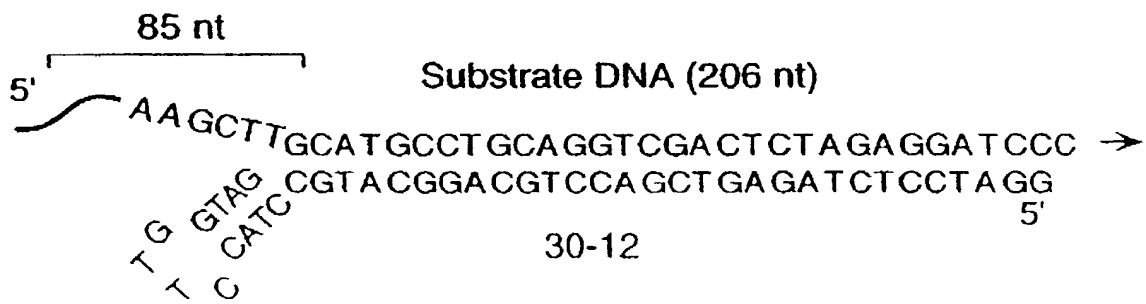
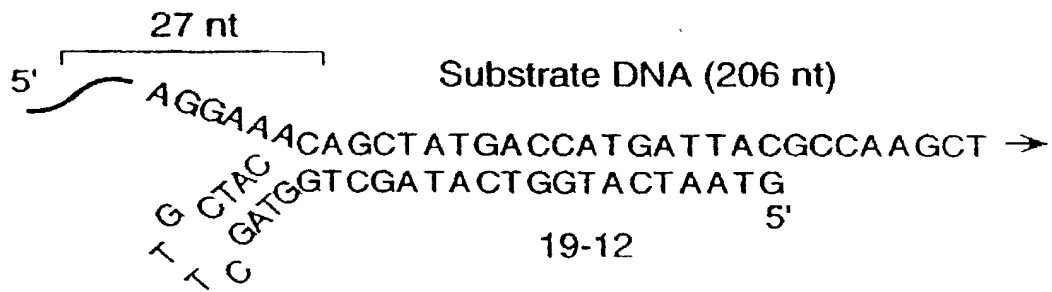


FIG. 12A



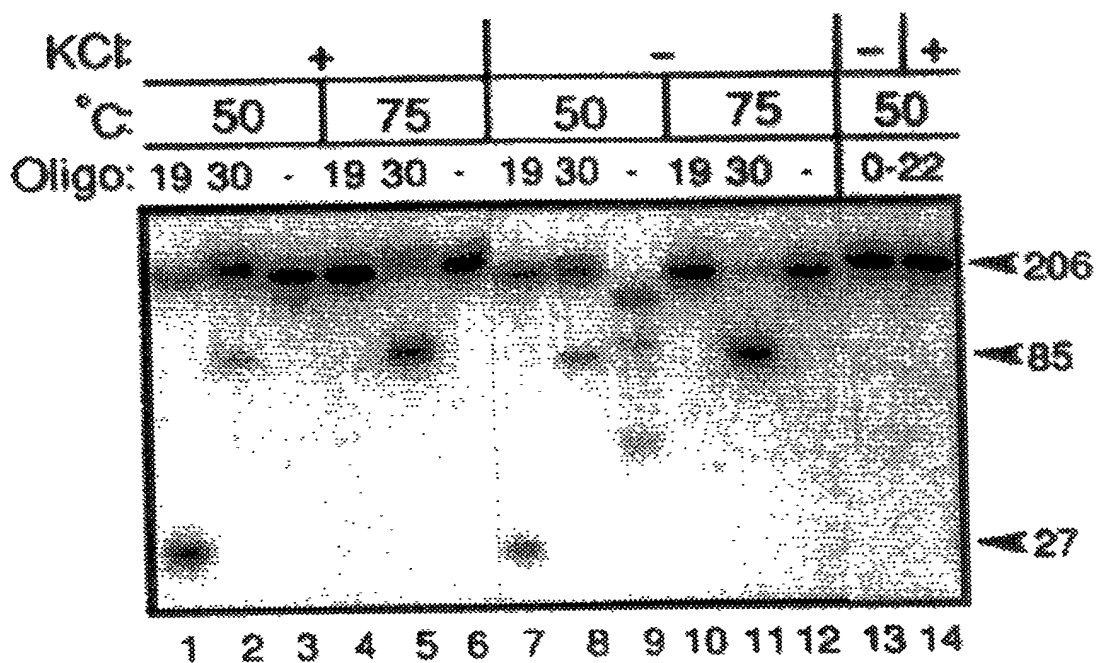


FIG. 12B

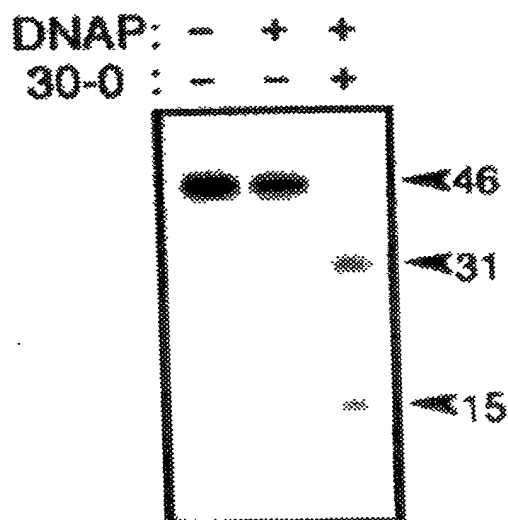


FIG. 13B

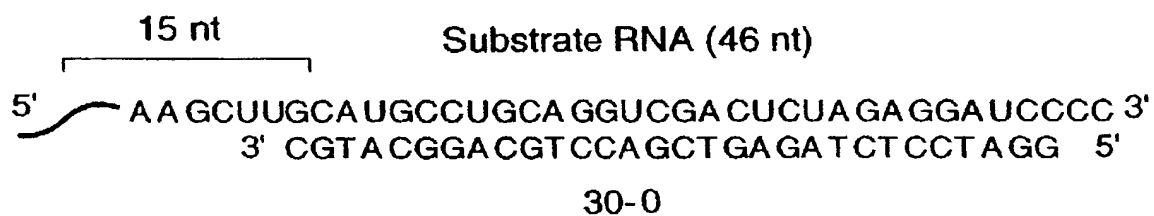


FIG. 13A

FIG. 14B

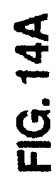
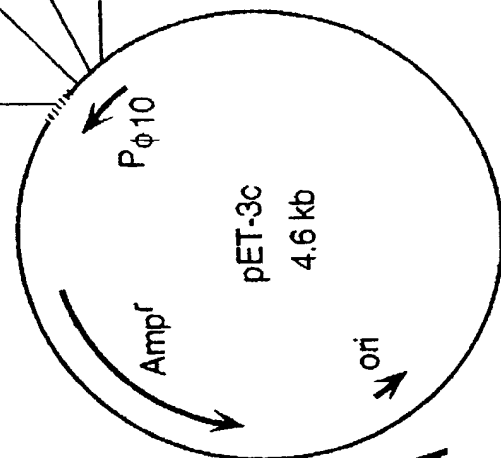
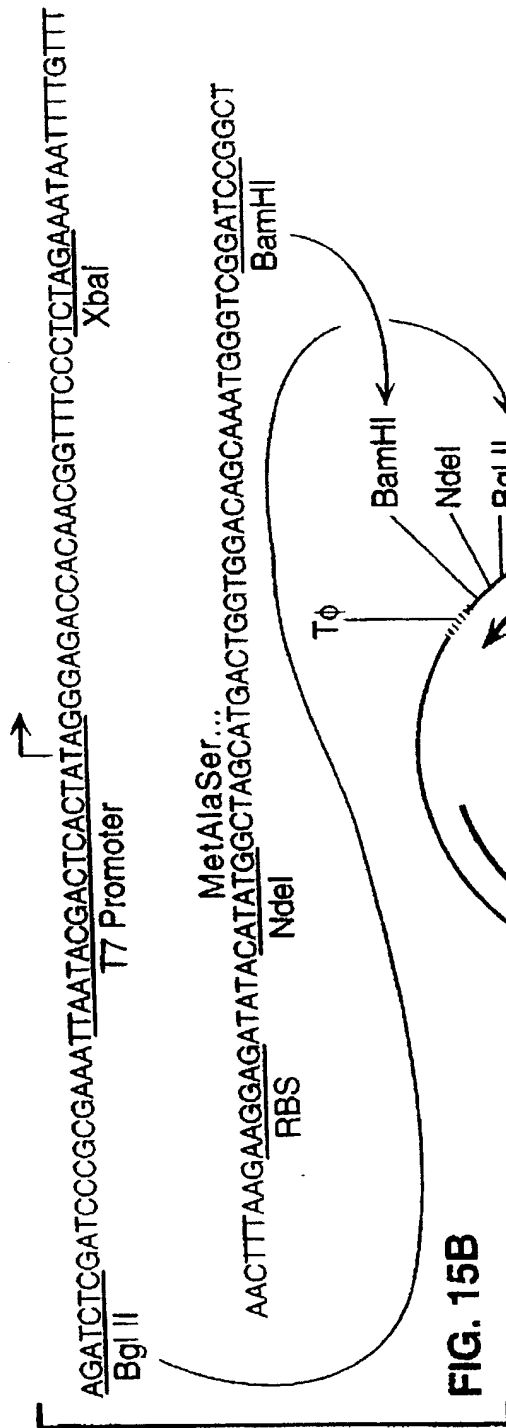


FIG. 14C



P_{φ10}: Bacteriophage T7 φ10 promoter
 T_φ: T7 φ Terminator

FIG. 15C

RBS: Ribosome binding site

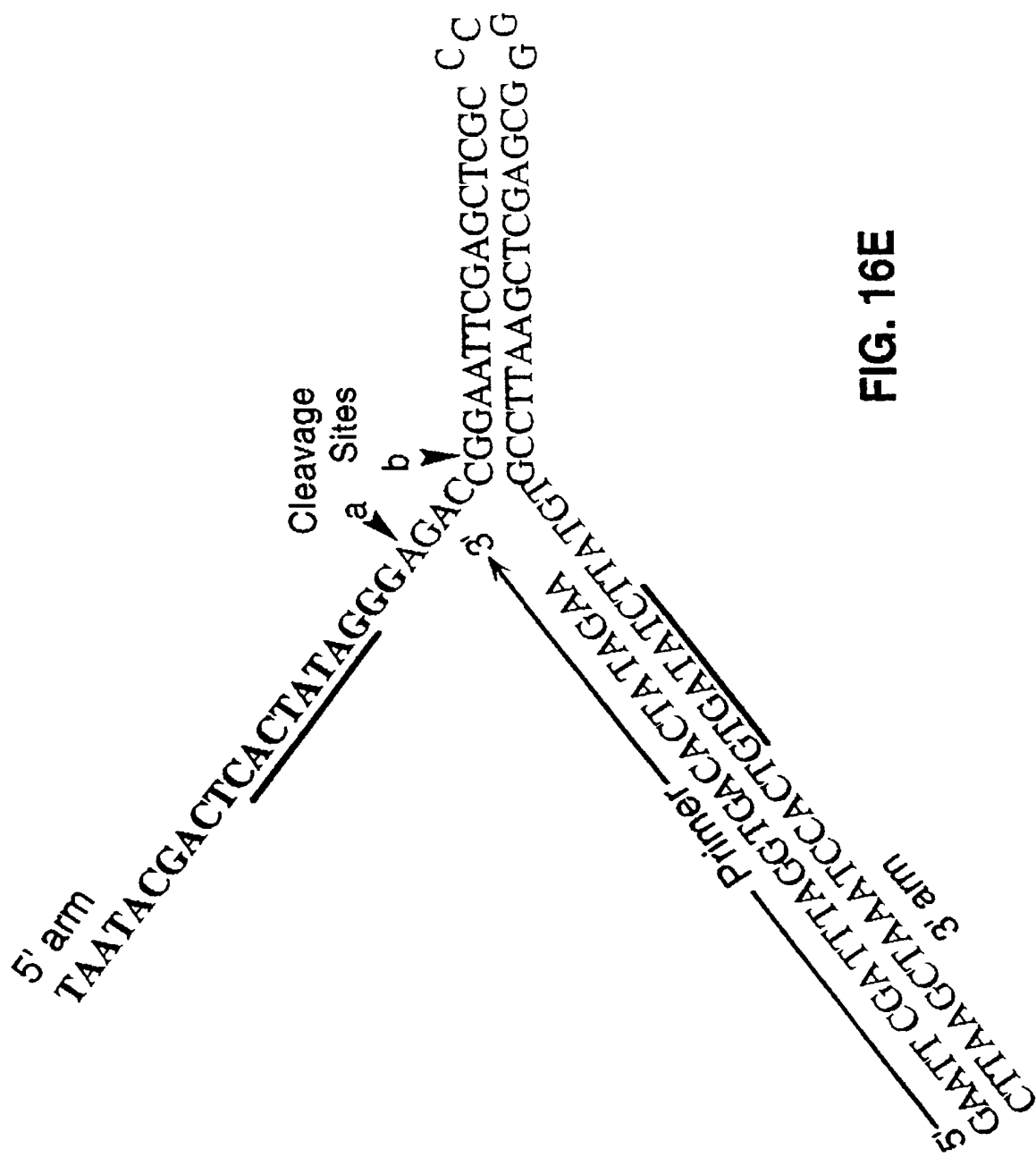


FIG. 16E

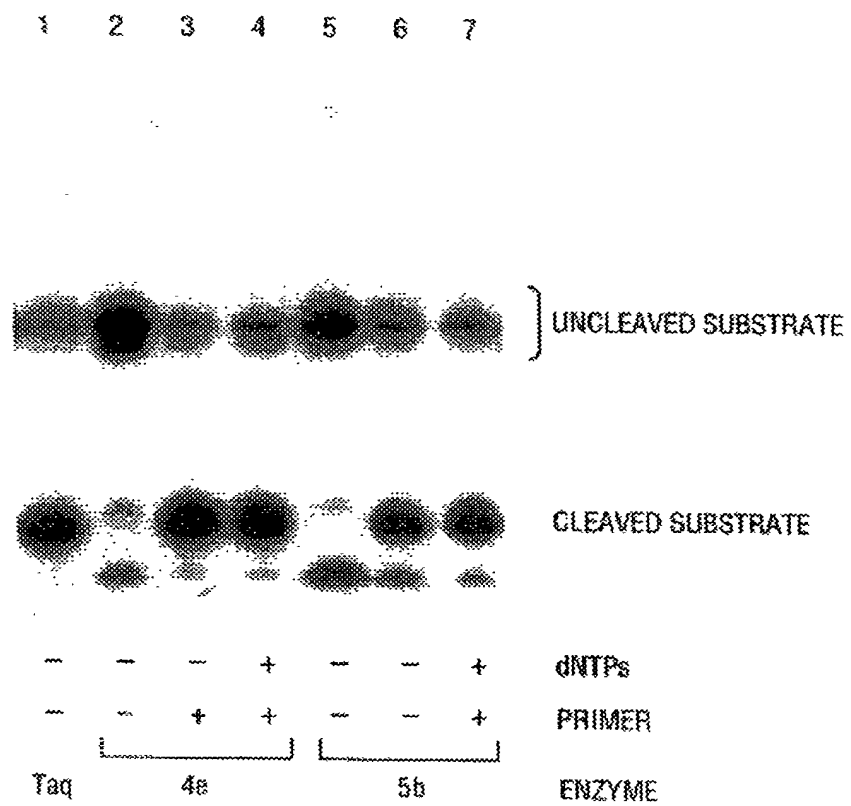


FIG. 17

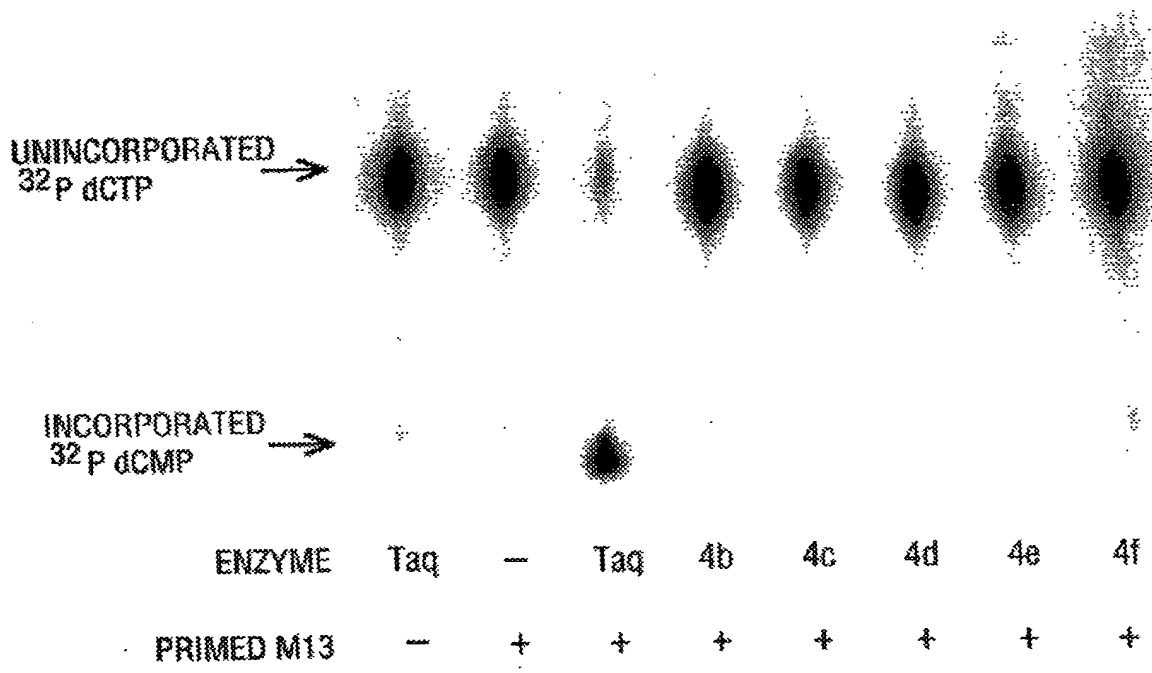


FIG. 18

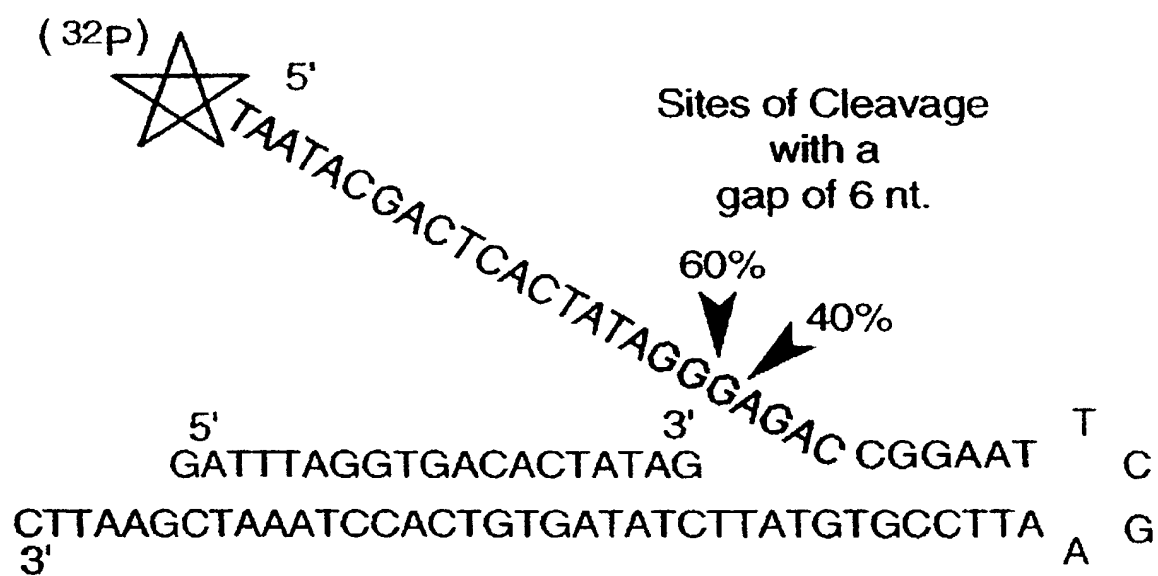
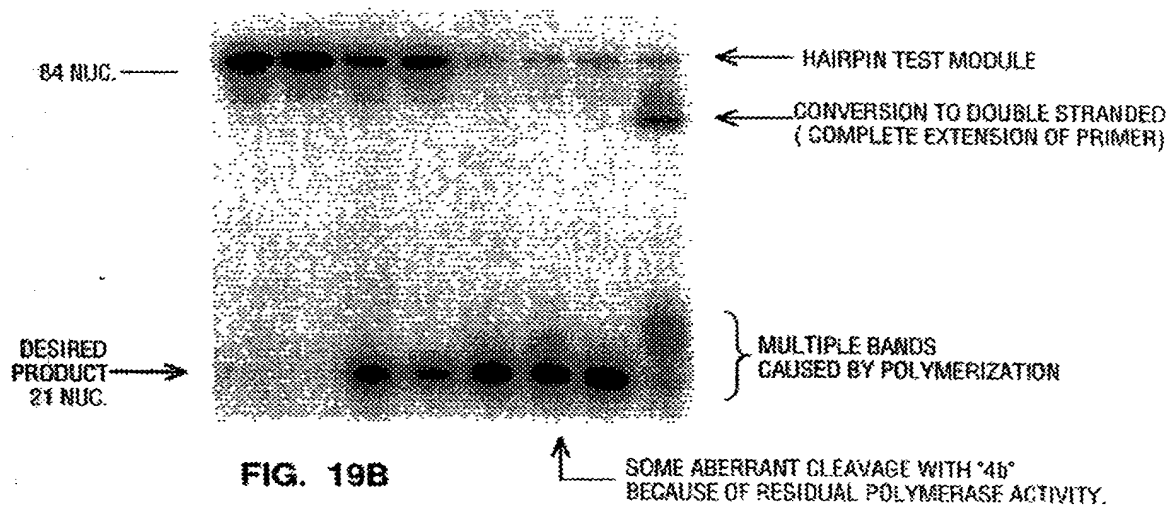
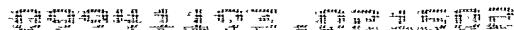


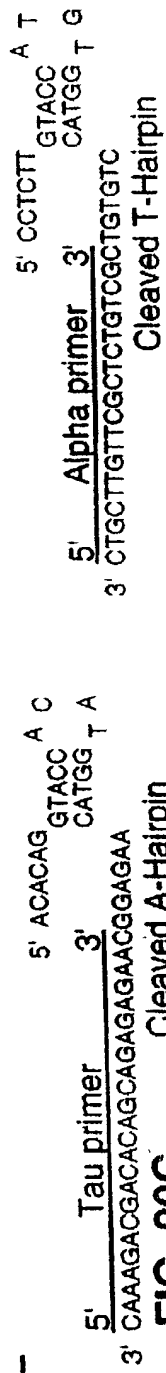
FIG. 19A

		4d		*4b*		UNMODIFIED		
		NO POL. ACTIVITY		2 PT. MUTATION SMALL ACTIVITY		DNAP Tag		
1	2	3	4	5	6	7	8	
		-	+	-	+	-	+	dNTP





Sequence of alpha primer:
5' GACGAACAAGCGAGACAGCG 3'



5' GTTCTGCTGTGTGCTCTCTCTTGCCCTCTTTGACCATGTGGTACCTGTGTGCGTGTCTGCTTGGTC 3'
3' CAAAGACGACACAGCAGAGAGACGGAGAACATGTTACCATGGACACAGCGACAGAGCGAACAAGCAGGC 5'

Restriction sites (indicated by vertical lines):

- BsmAI
- RsaI
- MnII
- NlaIII
- HgiCI
- RsaI/NlaIV
- KpnI
- BsmAI
- T-Hairpin
- A-Hairpin

FIG. 20D

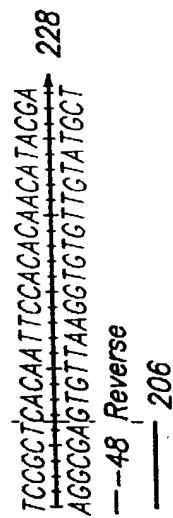
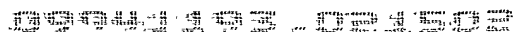


FIG. 21

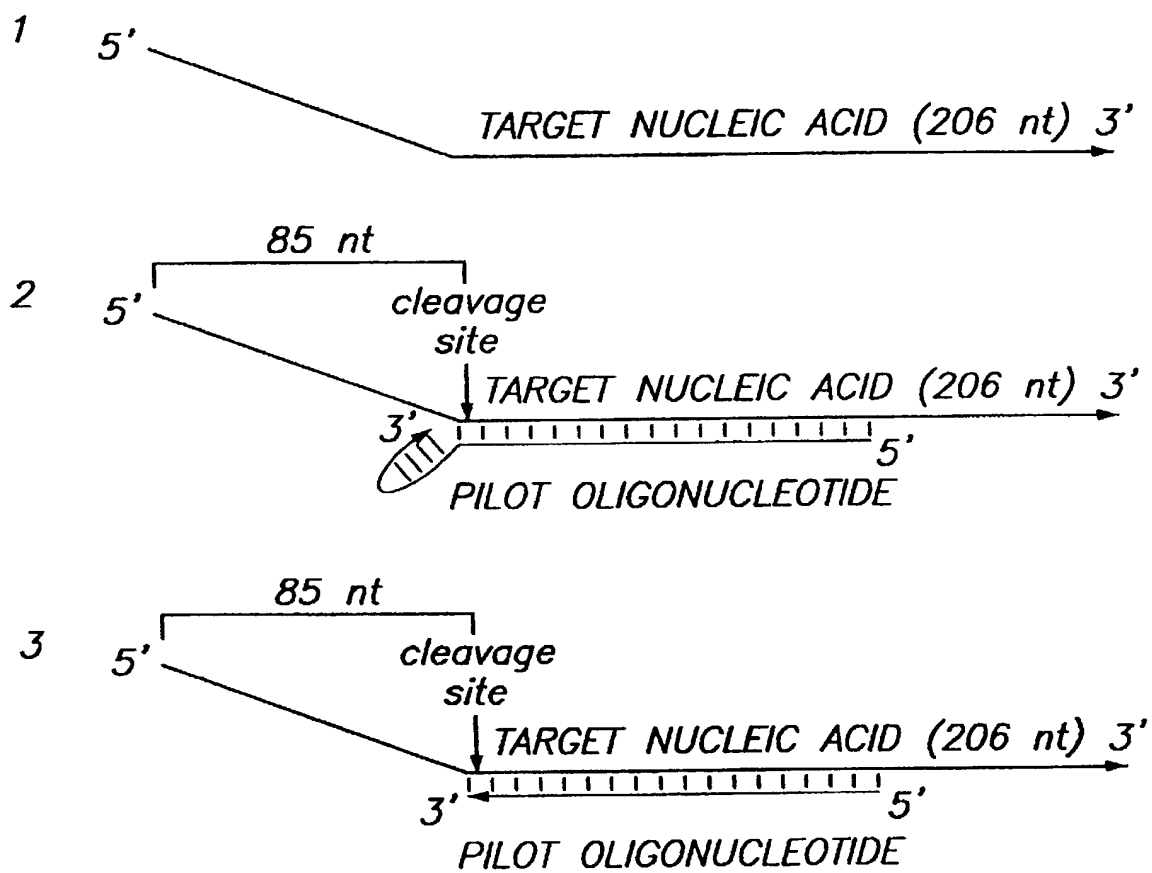


FIG. 22A

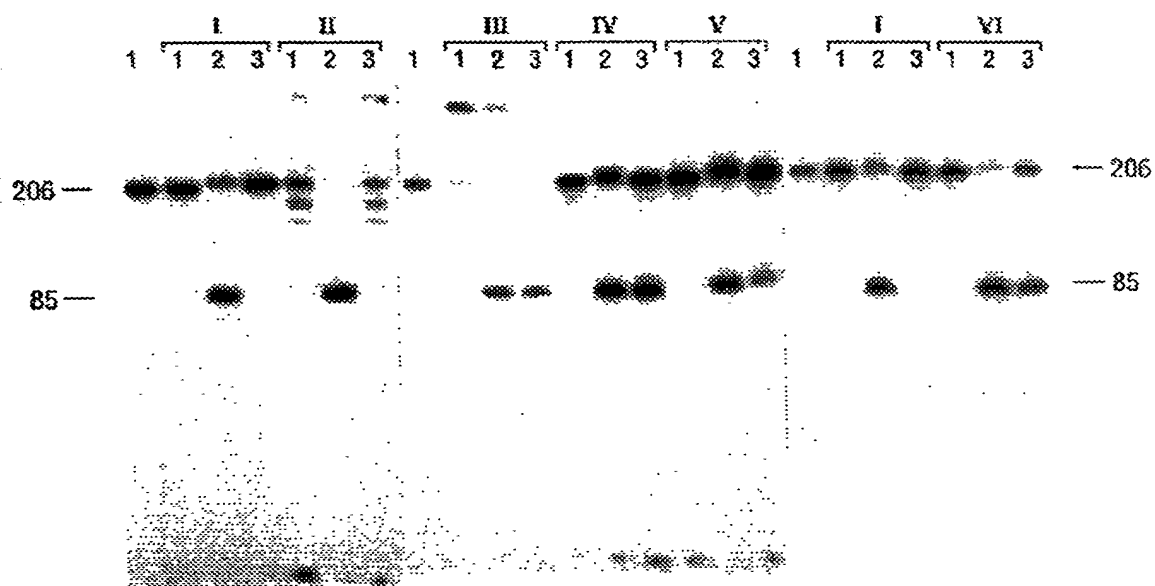


FIG. 22B

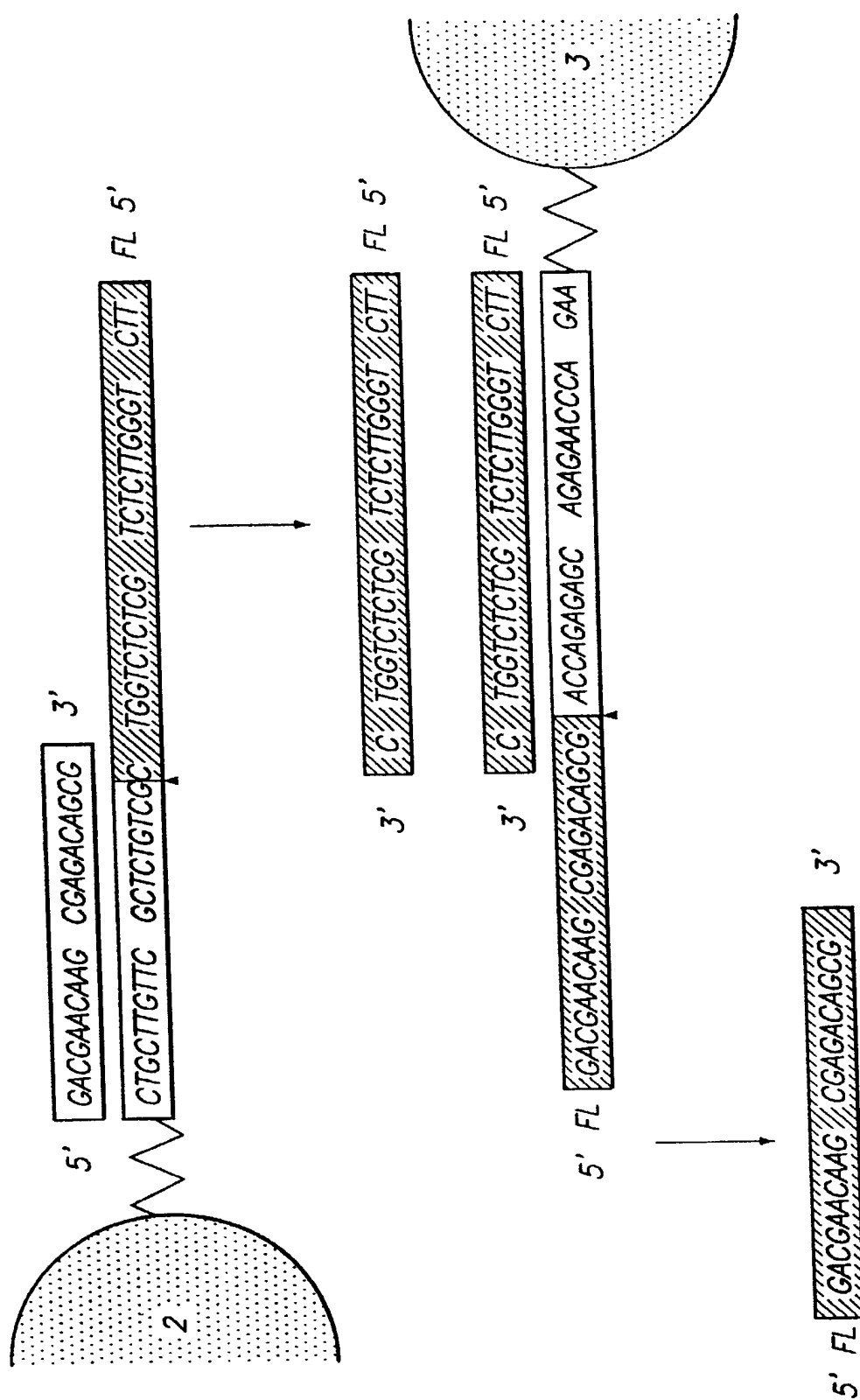


FIG. 23

[illegible]

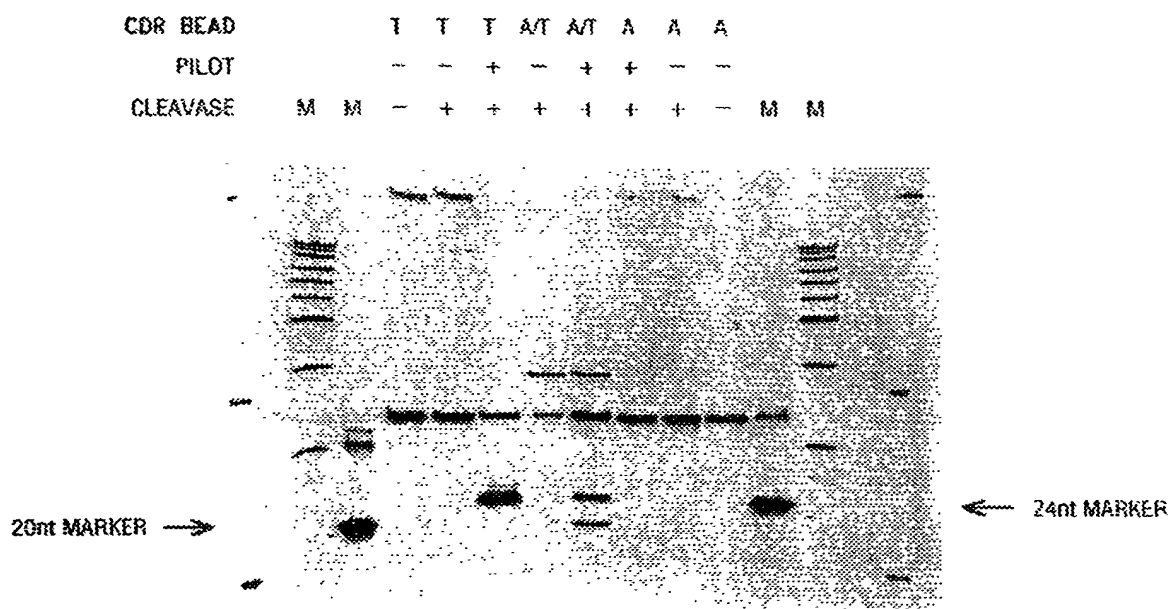


FIG. 24

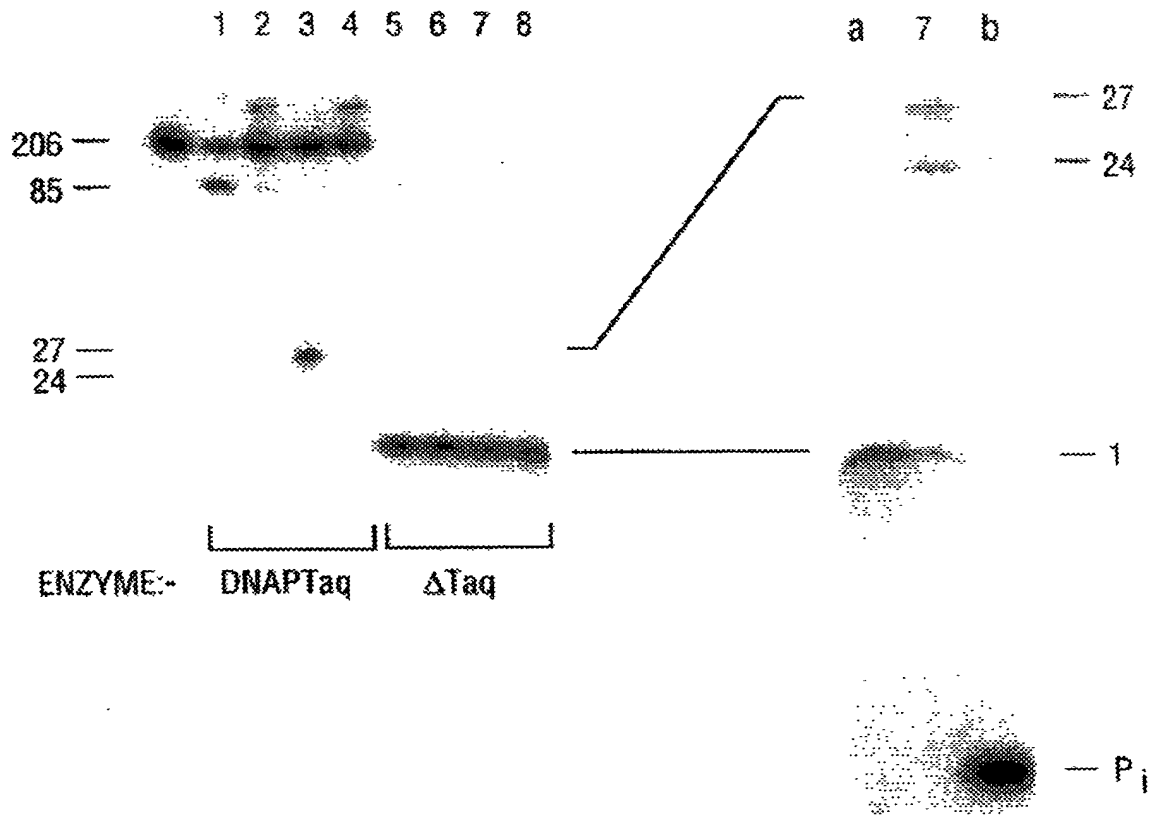


FIG. 25A

FIG. 25B

FIG. 26A

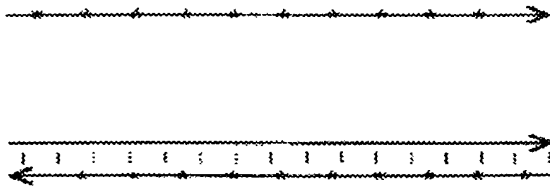
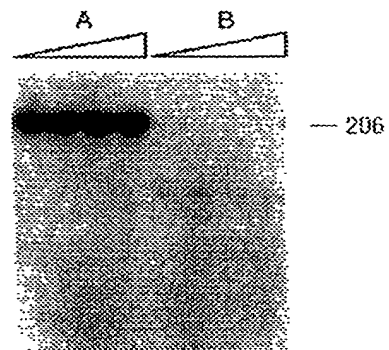


FIG. 26B

* :: 32p



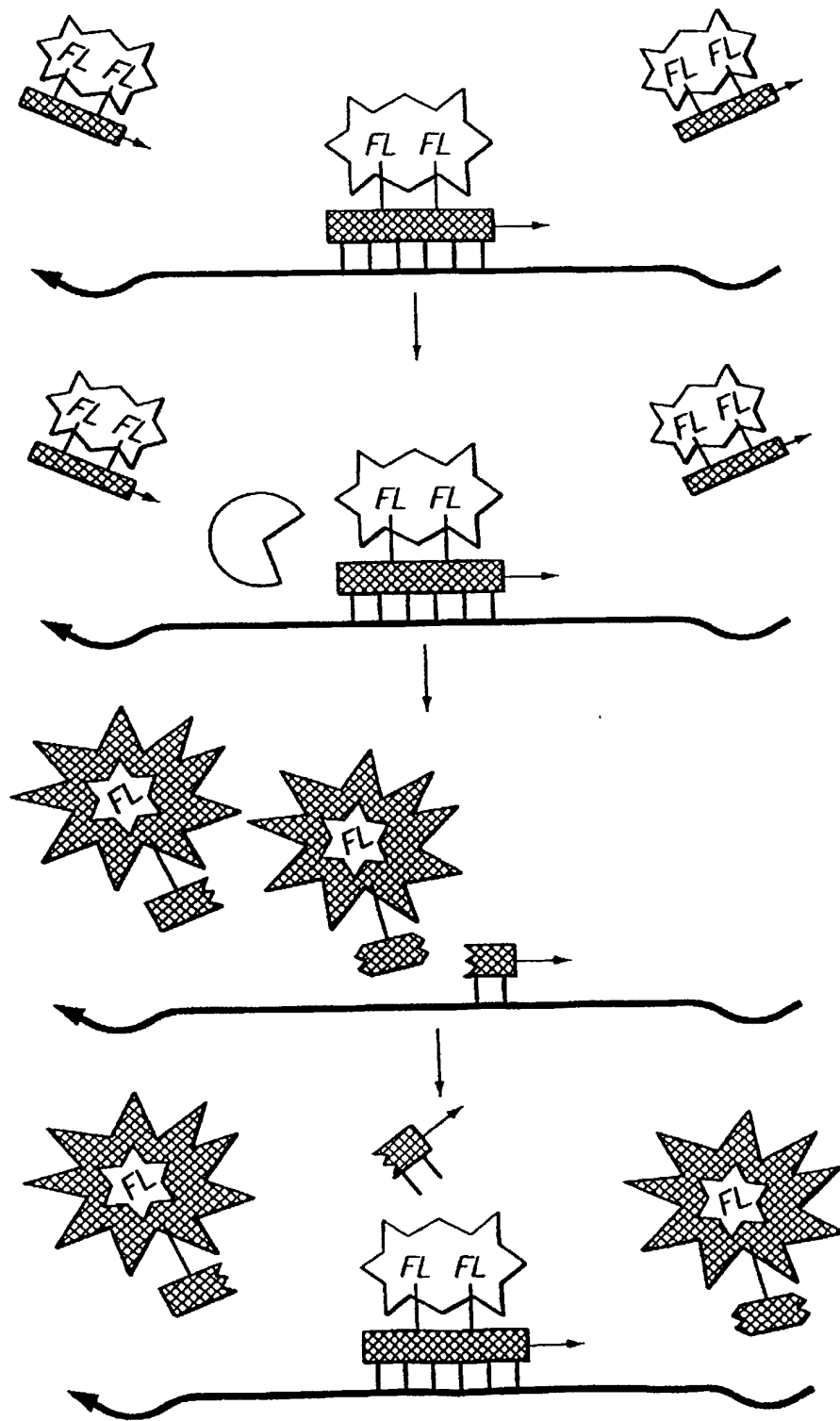


FIG. 27

The diagram shows a plasmid target, represented by a wavy line. A horizontal line segment is drawn across the middle of the plasmid, with a 5' end on the left and a 3' end on the right. A vertical line with an asterisk (*) is drawn at the 5' end of this segment. Below the plasmid, the text "PLASMID TARGET" is written. Above the plasmid, three arrows point away from the 5' end of the segment, each starting from an asterisk (*). Below the plasmid, the text "* = ^{32}P 5' TERMINAL PHOSPHATE" is written.

FIG. 28A

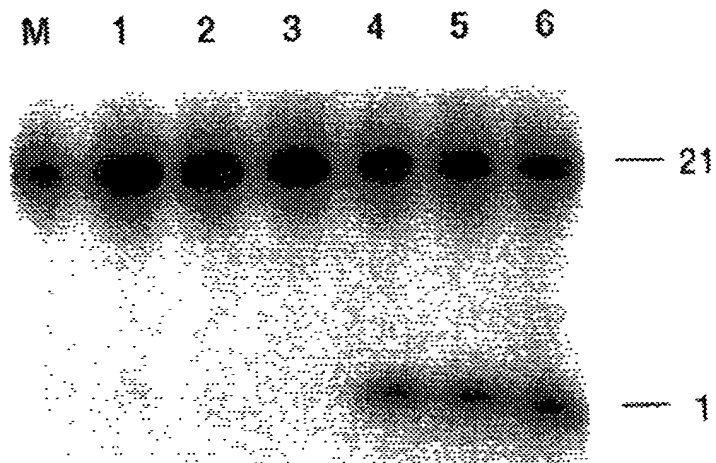


FIG. 28B

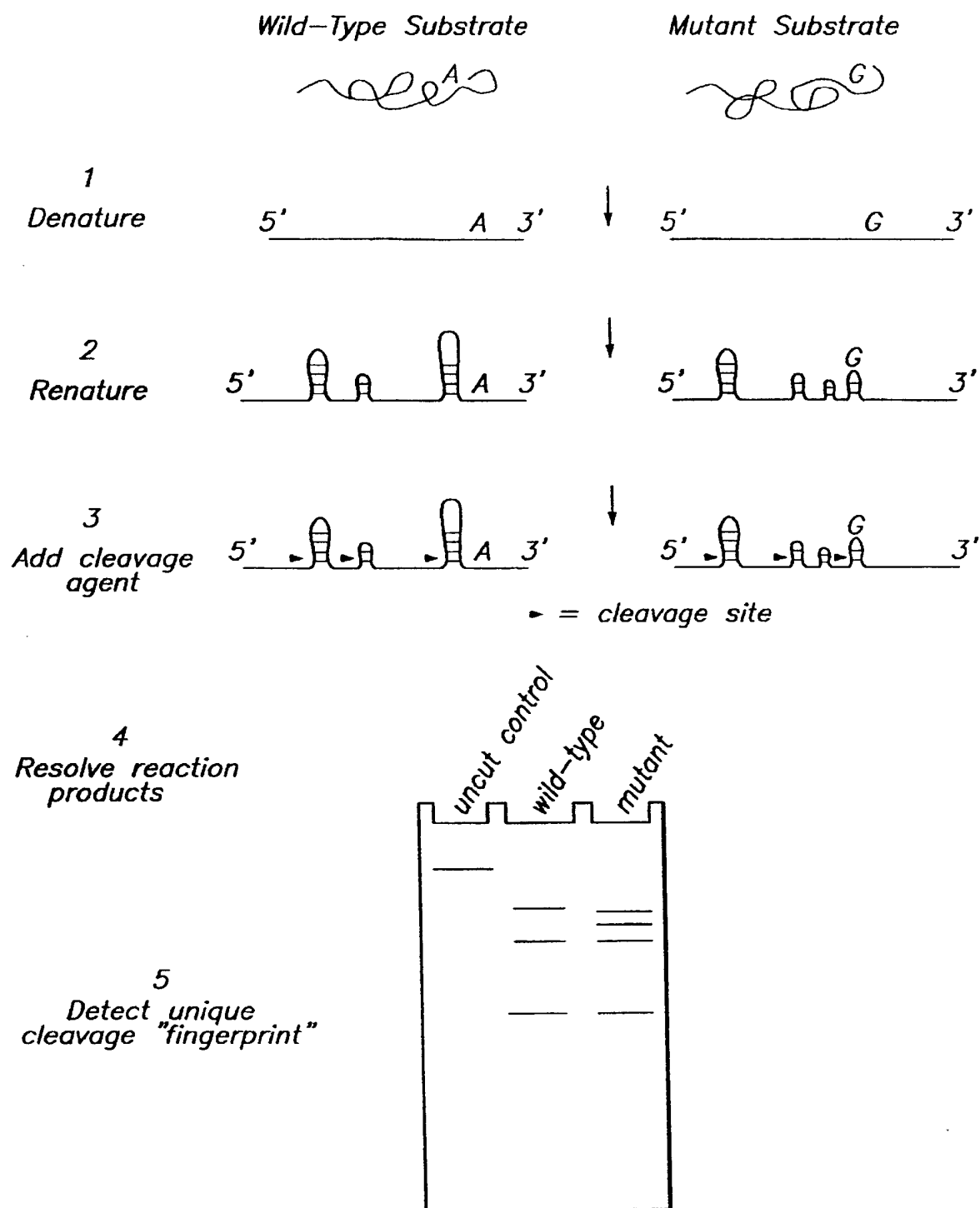


FIG. 29

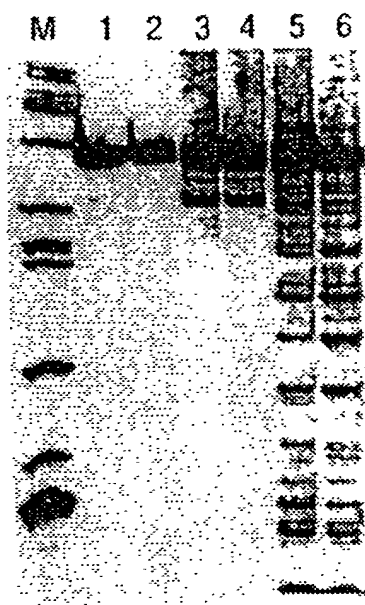


FIG. 30

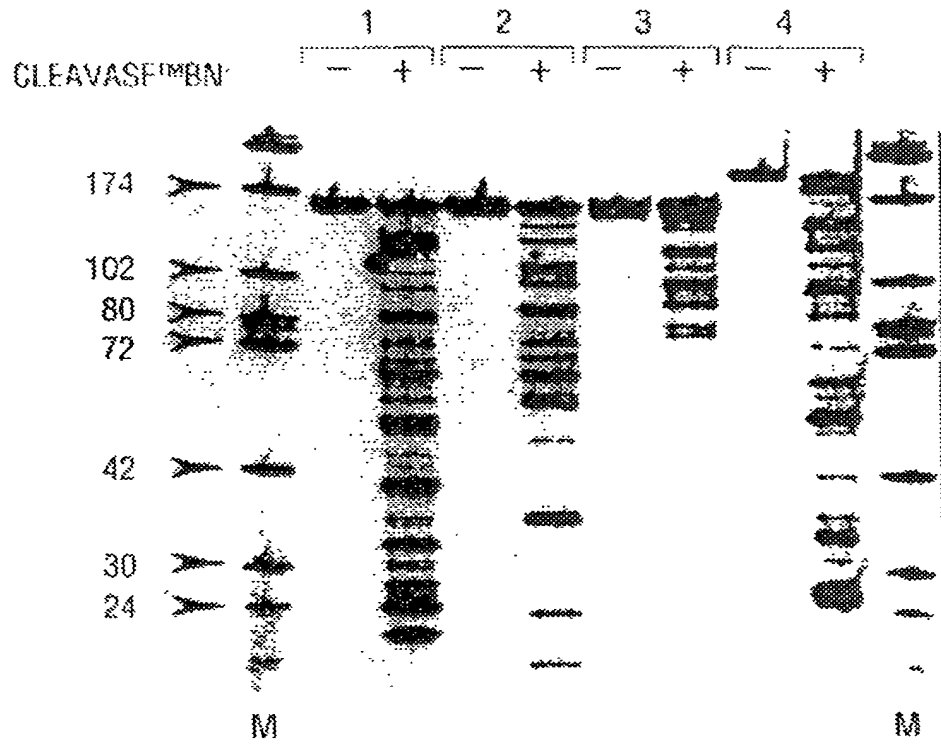


FIG. 31

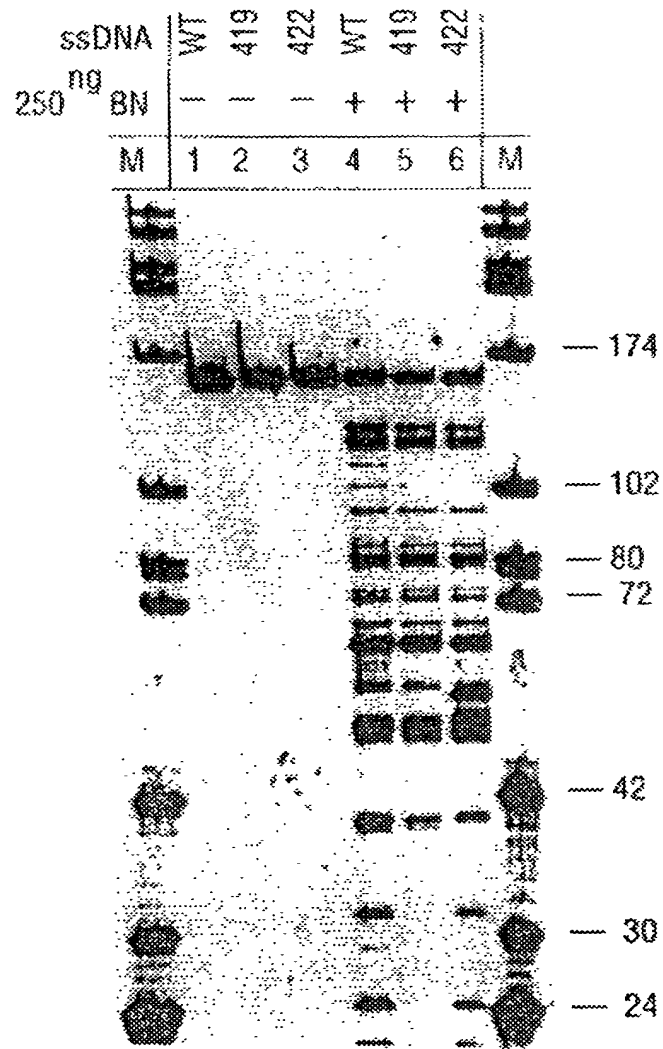


FIG. 32

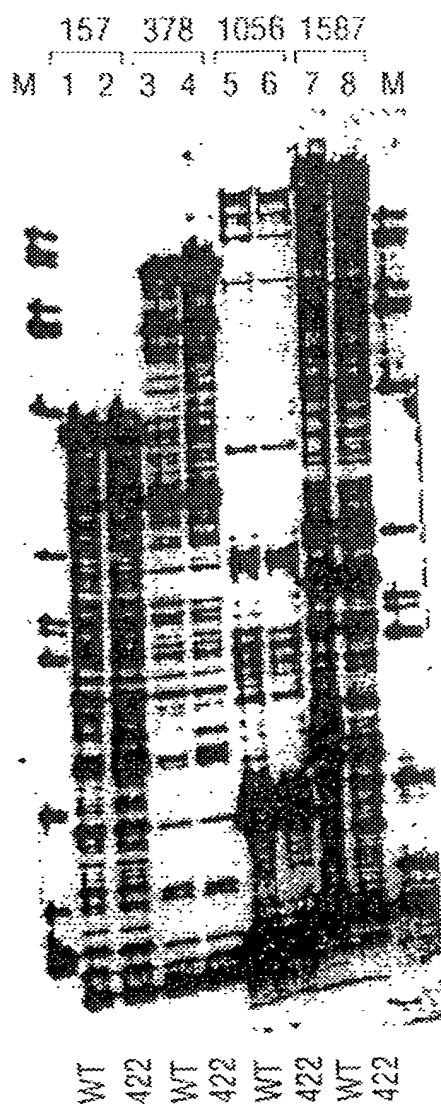


FIG. 33

FIG. 34

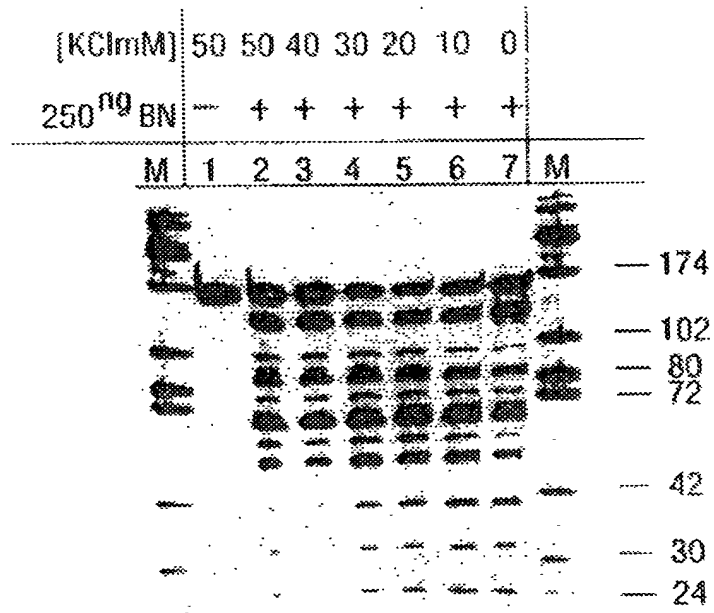


FIG. 35

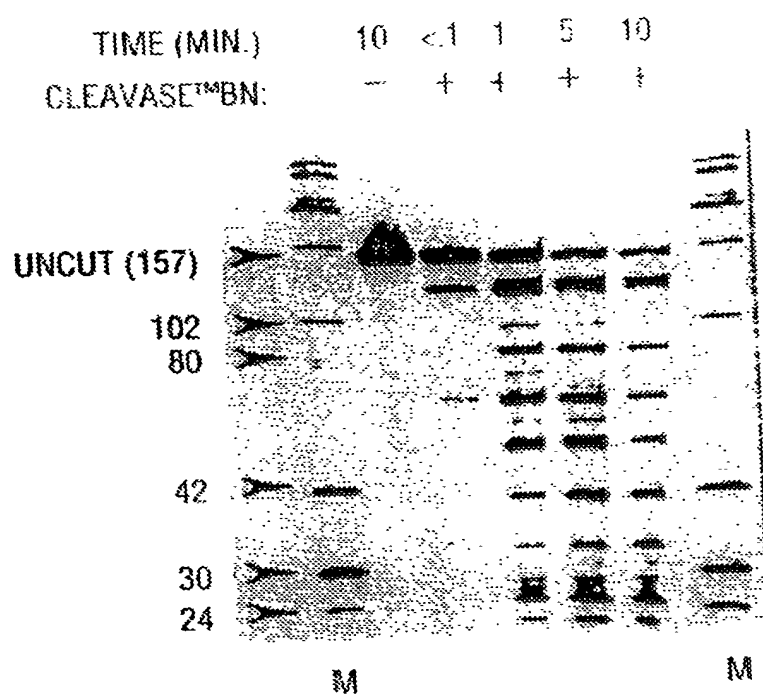


FIG. 36

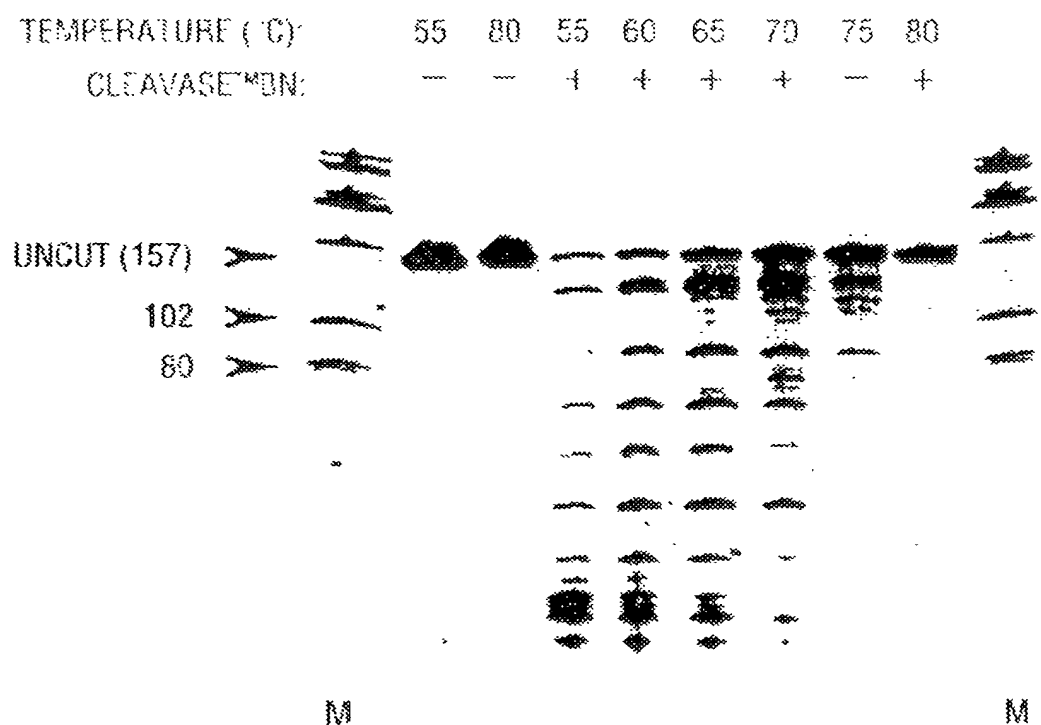


FIG. 37

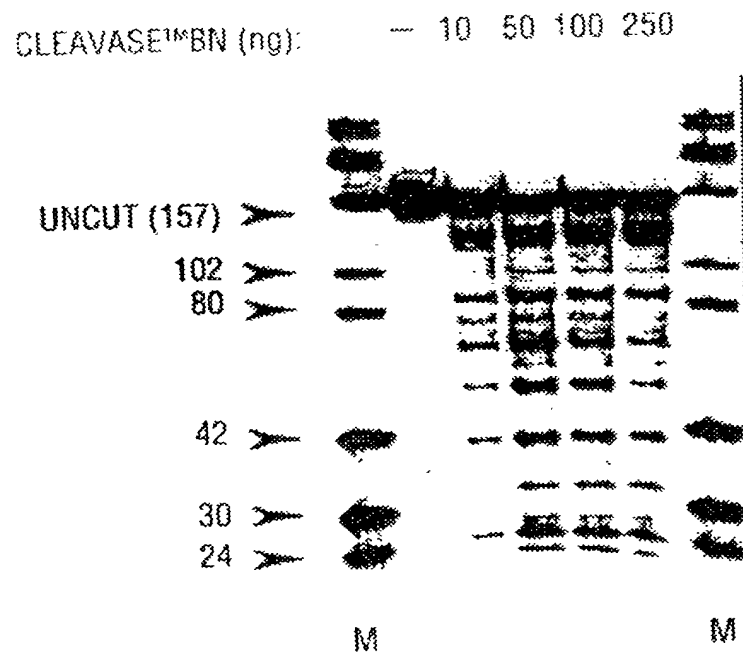


FIG. 38

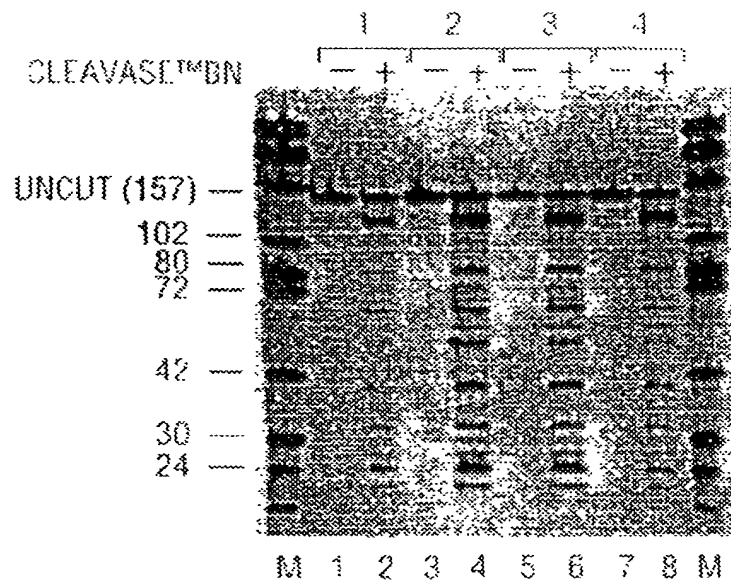


FIG. 39

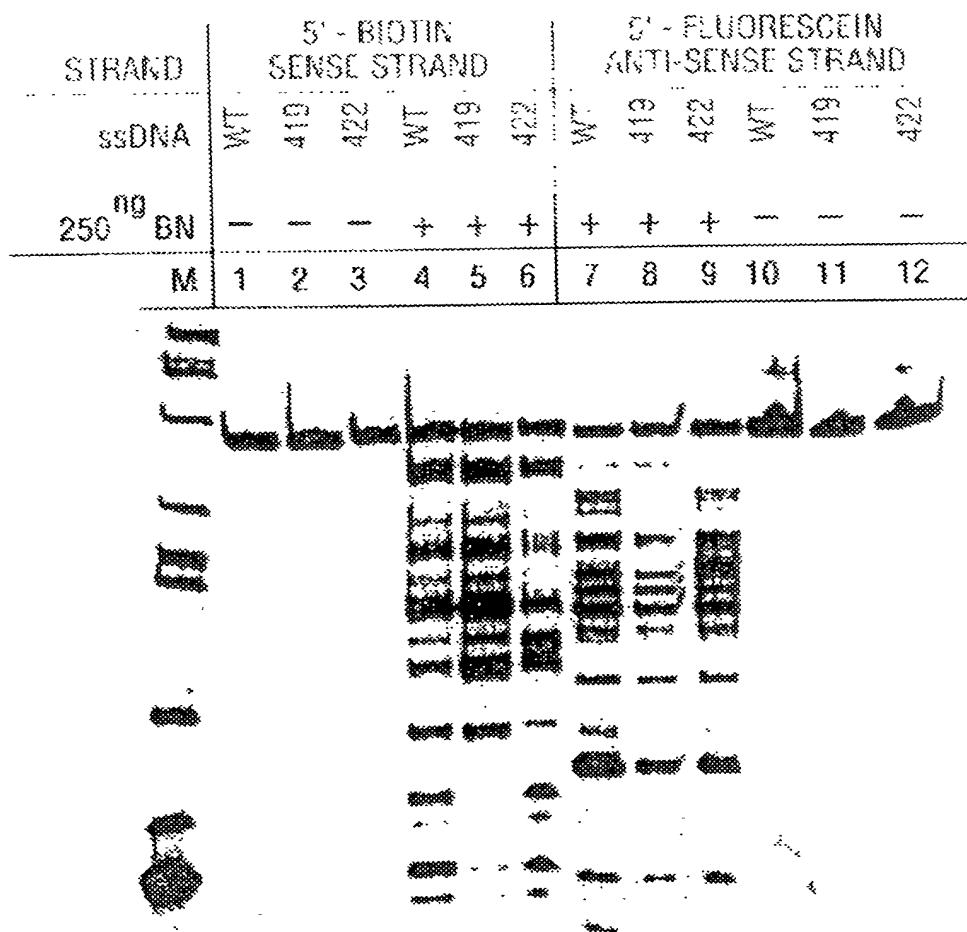


FIG. 40

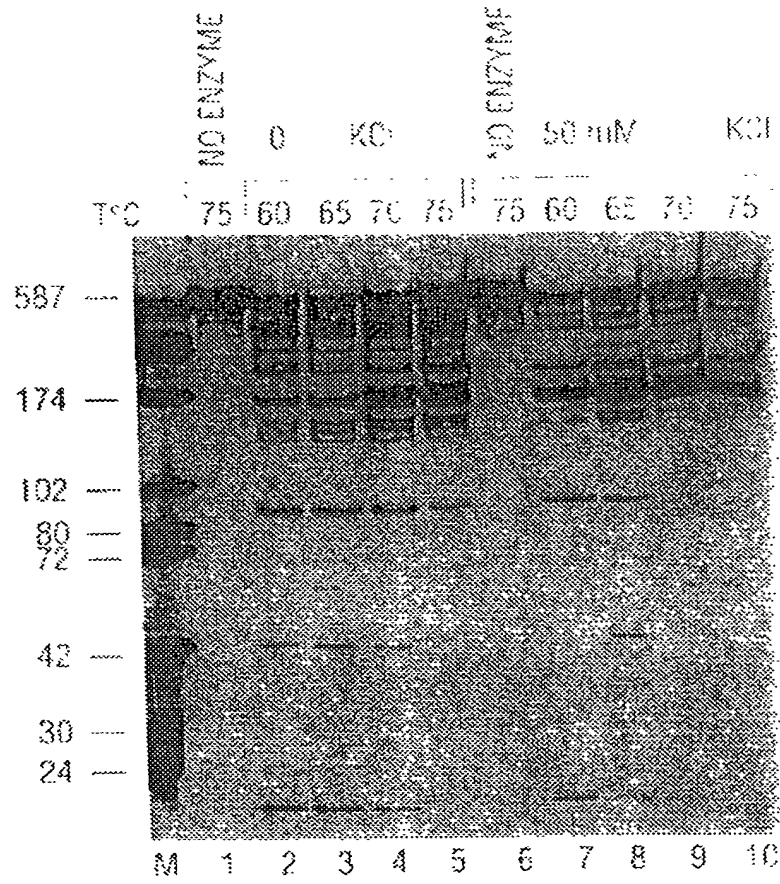


FIG. 41

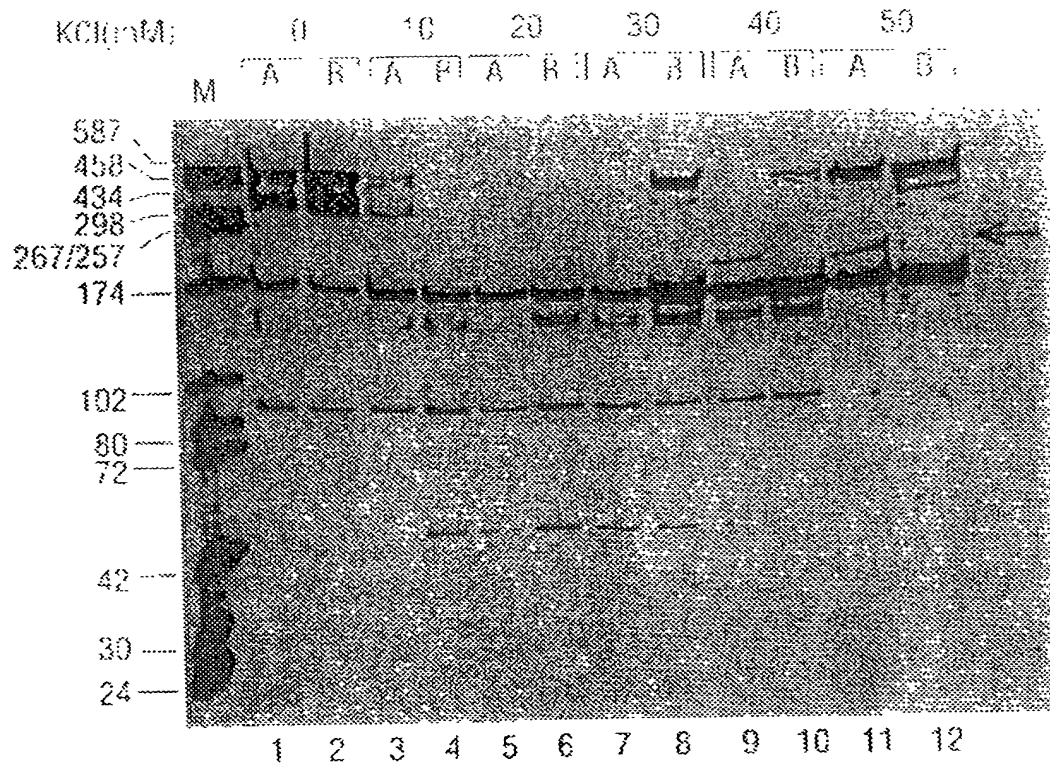


FIG. 42

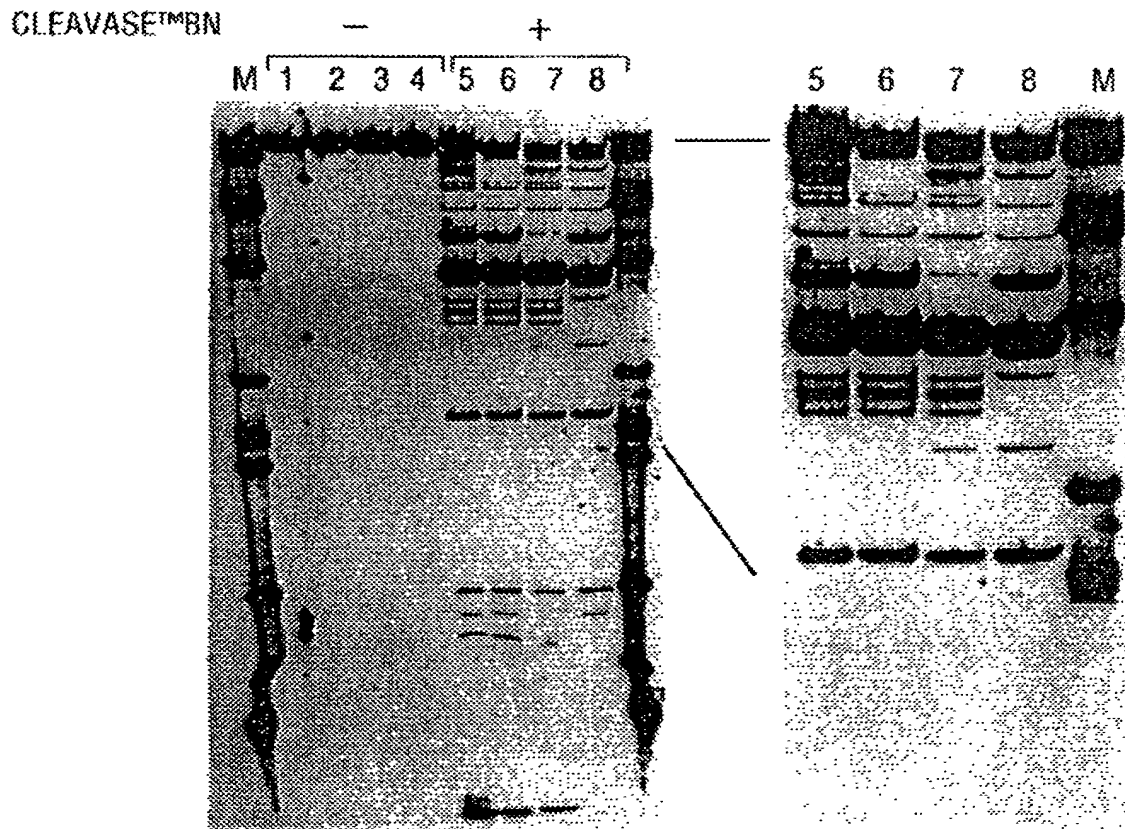
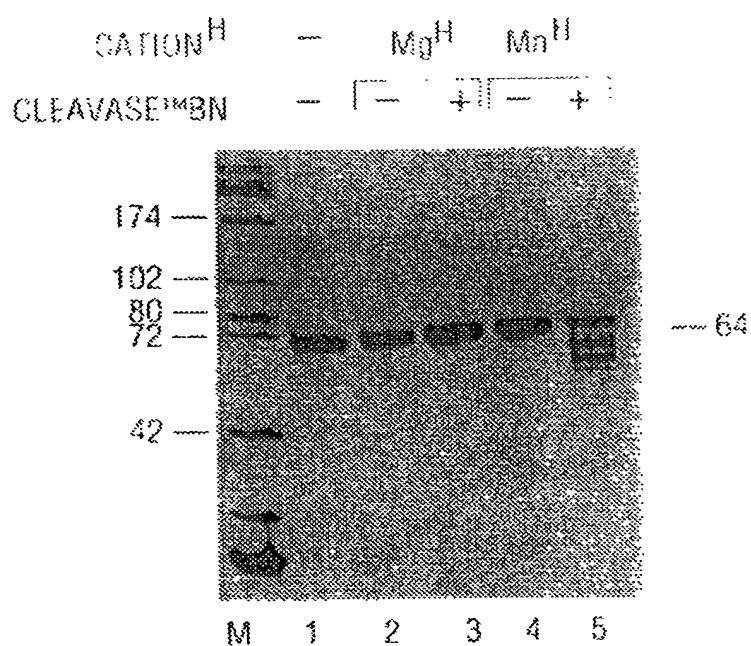


FIG. 43



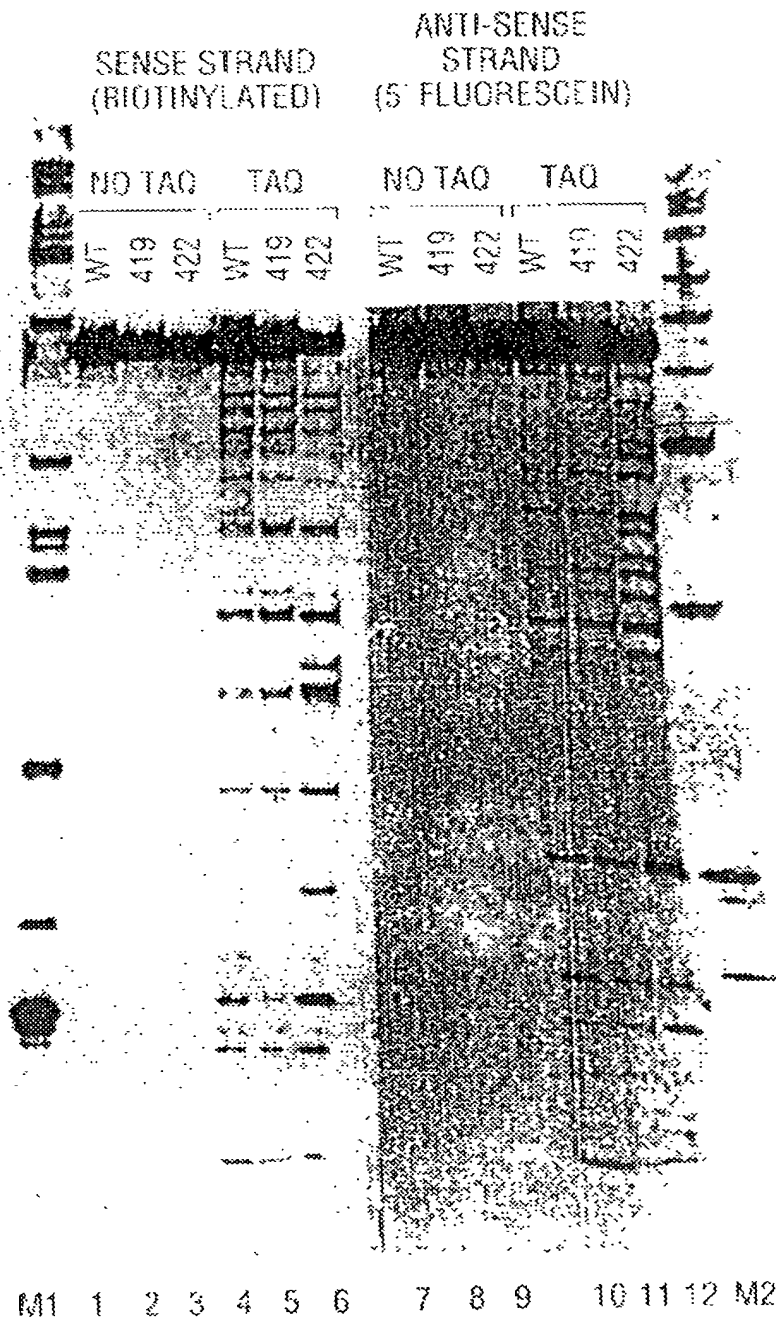


FIG. 46

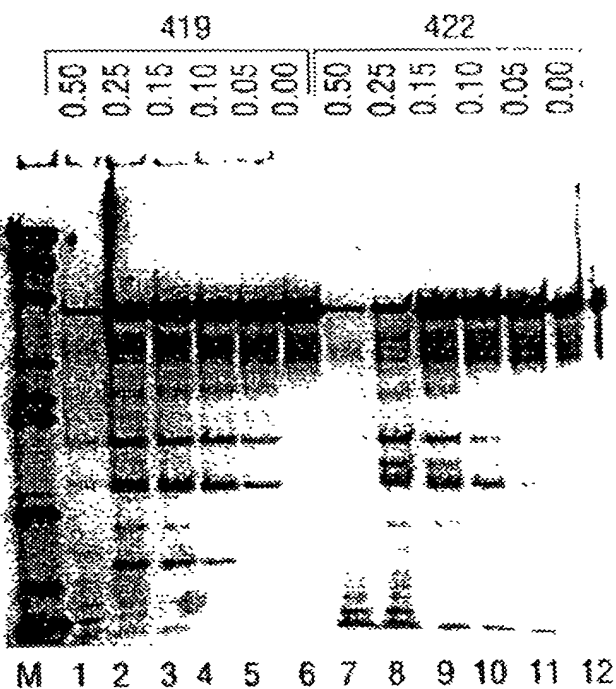


FIG. 47

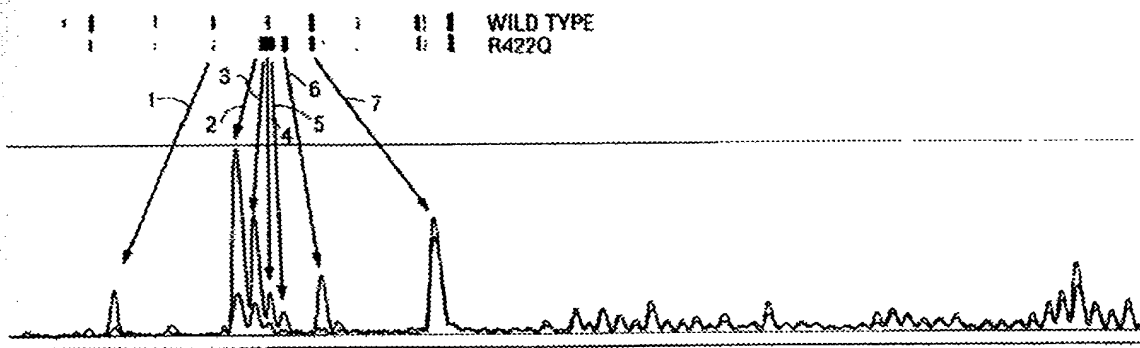


FIG. 48

L.100.8-1
(SEQ ID NO: 76) 5'GGCTGACAAGAAGGAAACTCGCTGAGACAGCAGGGGACTTTCCACAAGGGG
3'CCGACTGTTCTTCCCTTGAGCGACTCTGTCGTCCCTGAAAGGTGTTCCCC

L.46.16-10
(SEQ ID NO: 77) 5'GGCTGACAAGAAGGAAACTCGCTGAGATAGCAGGGGACTTTCCACAAGGGG
3'CCGACTGTTCTTCCCTTGAGCGACTCTATCGTCCCTGAAAGGTGTTCCCC

L.46.16-12
(SEQ ID NO: 78) 5'GGCTGACAAGAAGGAAACTCGCTGAGATAGCAGGGGACTTTCCACAAGGGG
3'CCGACTGTTCTTCCCTTGAGCGACTCTATCGTCCCTGAAAGGTGTTCCCC

L19.16-3
(SEQ ID NO: 79) 5'GGCTGACAAGAAGGAAACTCGCTGAGACAGCAGGGGACTTTCCACAAGGGG
3'CCGACTGTTCTTCCCTTGAGCGACTCTGTCGTCCCTGAAAGGTGTTCCCC

L.CEM/251
(SEQ ID NO: 80) 5'GGCTGACAAGAAGGAAACTCGCTGAAACAGCAGGGGACTTTCCACAAGGGG
3'CCGACTGTTCTTCCCTTGAGCGACTTTGTCGTCCCTGAAAGGTGTTCCCC

L.36.8-3
(SEQ ID NO: 81) 5'GGCTGACAAGAAGGAAACTCGCTGAGACAGCAGGGGACTTTCCACAAGGGG
3'CCGACTGTTCTTCCCTTGAGCGACTCTGTCGTCCCTGAAAGGTGTTCCCC

FIG. 49A

CGCTGACAAGAAGGAAACTCGCTGAGACAGCAGGGGACTTTCCACAAGGGG

Accession	Sequence	Length
L.100.8-1	5'TGATGTATAAATATCACTGCATTTTCGCTCTGTATTTCAGTCGCTCTGCGGA 3'ACTACATAATTTATAGTGACGTAAGCGGAGACATAAGTCAGCGAGACGCCT	150
L.46.16-10	5'TGATGTATAAATATCACTGCATTTTCGCTCTGTATTTCAGTCGCTCTGCGGA 3'ACTACATAATTTATAGTGACGTAAGCGGAGACATAAGTCAGCGAGACGCCT	
L.46.16-12	5'TGGTGTATAAATATCACTGCATTTTCGCTCTGTATTTCAGTCGCTCTGCGGA 3'ACCACATAATTTATAGTGACGTAAGCGGAGACATAAGTCAGCGAGACGCCT	
L.19.16-3	5'TGATGTATAAATATCACTGCATTTTCGCTCTGTATTTCAGTCGCTCTGCGGA 3'ACTACATAATTTATAGTGACGTAAGCGGAGACATAAGTCAGCGAGACGCCT	
L.CEM/251	5'TGATGTATAAATATCACTGCATTTTCGCTCTGTATTTCAGTCGCTCTGCGGA 3'ACTACATAATTTATAGTGACGTAAGCGGAGACATAAGTCAGCGAGACGCCT	
L.36.8-3	5'TGATGTATAAATATCACTGCATTTTCGCTCTGTATTTCAGTCGCTCTGCGGA 3'ACTACATAATTTATAGTGACGTAAGCGGAGACATAAGTCAGCGAGACGCCT	

FIG. 49C

[illegible]

L.100.8-1 200
GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG
CTCCGACCGTCTAACTCGGGACCCCTCCAAGAGAGGTCGTGATCGTCCATC

L.46.16-10
GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG
CTCCGACCGTCTAACTCGGGACCCCTCCAAGAGAGGTCGTGATCGTCCATC

L.46.16-12
GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG
CTCCGACCGTCTAACTCGGGACCCCTCCAAGAGAGGTCGTGATCGTCCATC

L.19.16-3
GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG
CTCCGACCGTCTAACTCGGGACCCCTCCAAGAGAGGTCGTGATCGTCCATC

L.CEM/251
GAGGCTGGCAGATTGAGCCCTGGGAGGTTCTCTCCAGCACTAGCAGGTAG
CTCCGACCGTCTAACTCGGGACCCCTCCAAGAGAGGTCGTGATCGTCCATC

L.36.8-3
GAGGCTGGCAGATTGAGCCCTAGGAGGTTCTCTCCAGCACTAGCAGGTAG
CTCCGACCGTCTAACTCGGGATCCTCCAAGAGAGGTCGTGATCGTCCATC

FIG. 49D

200 199 198 197 196 195 194 193 192 191 190 189 188 187 186 185 184 183 182 181 180 179 178 177 176 175 174 173 172 171 170 169 168 167 166 165 164 163 162 161 160 159 158 157 156 155 154 153 152 151 150 149 148 147 146 145 144 143 142 141 140 139 138 137 136 135 134 133 132 131 130 129 128 127 126 125 124 123 122 121 120 119 118 117 116 115 114 113 112 111 110 109 108 107 106 105 104 103 102 101 100 99 98 97 96 95 94 93 92 91 90 89 88 87 86 85 84 83 82 81 80 79 78 77 76 75 74 73 72 71 70 69 68 67 66 65 64 63 62 61 60 59 58 57 56 55 54 53 52 51 50 49 48 47 46 45 44 43 42 41 40 39 38 37 36 35 34 33 32 31 30 29 28 27 26 25 24 23 22 21 20 19 18 17 16 15 14 13 12 11 10 9 8 7 6 5 4 3 2 1

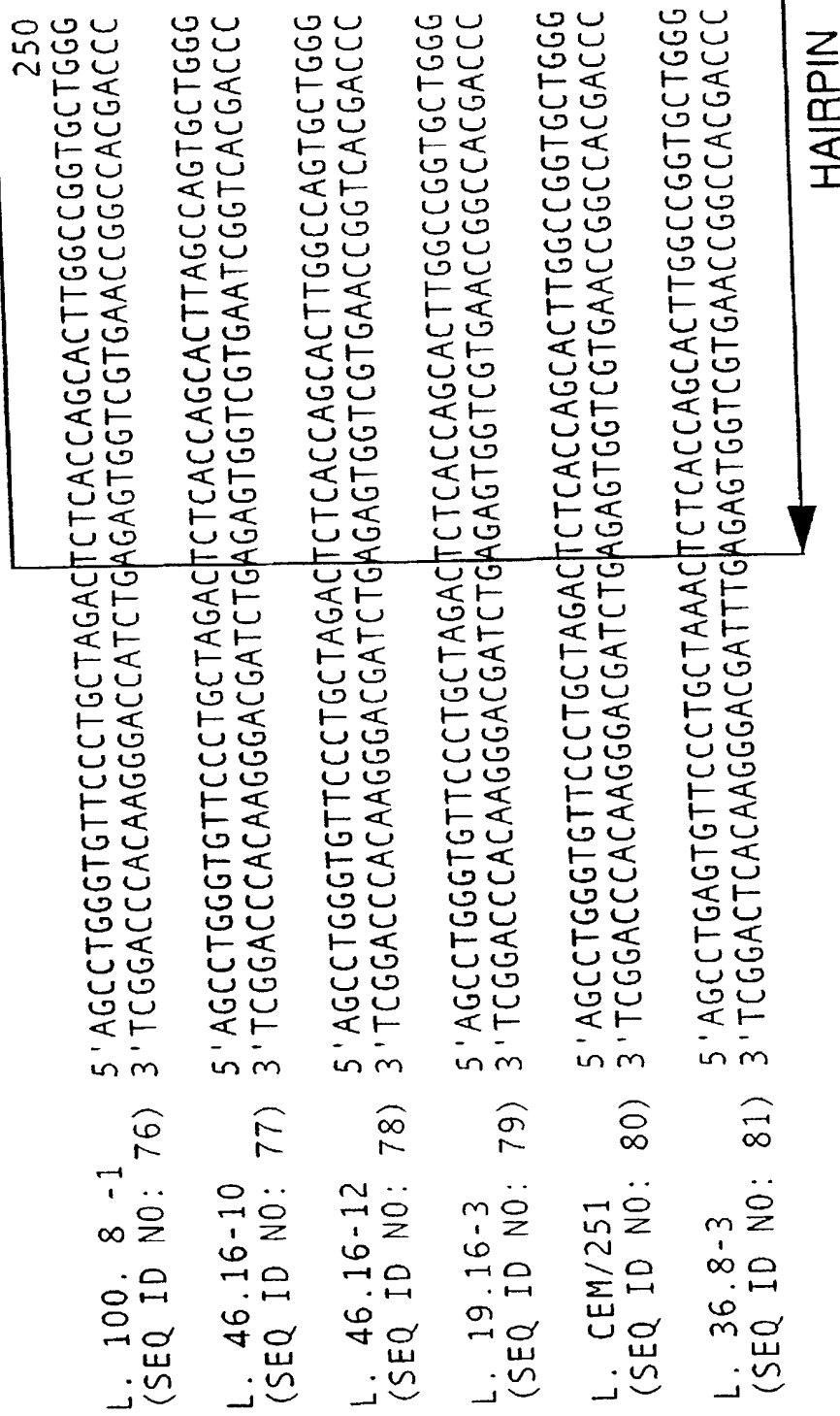


FIG. 49E

250 250 250 250 250 250

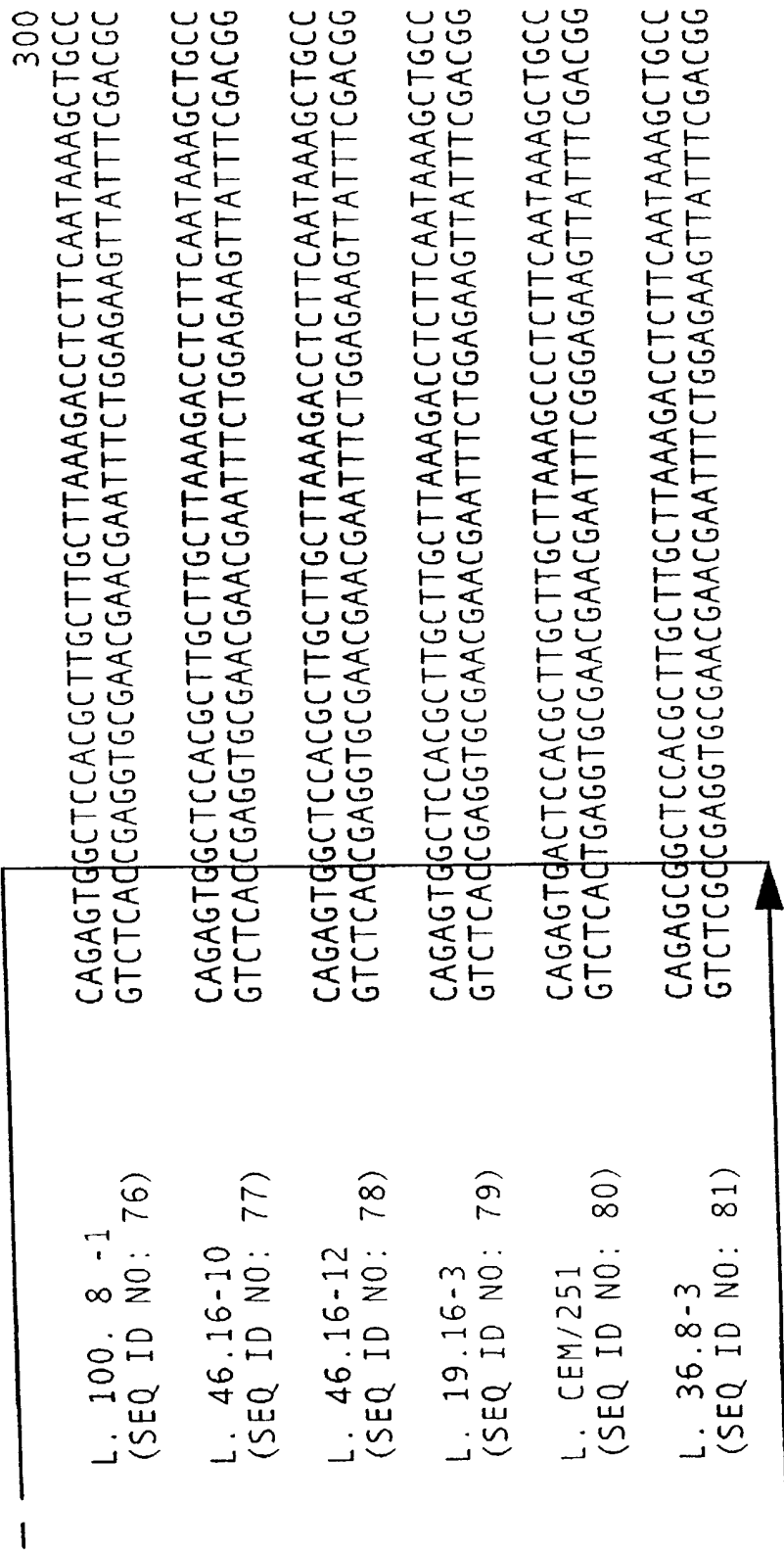


FIG. 49F

CGGTTTCTGGAGAAAGTTATTTTCGACGC

Accession	Sequence	Length
L.100.8-1	5'ATTTTAGAAGTAGGCCAGTGTGTGTTCCCATCTCTCCTAGCCGCCGCTG 3'TAAATCTTCATCCGGTCACACACACAAAGGTAGAGGATCGCGCGGAC	350 G 3' C 5'
L.46.16-10	5'ATTTTAGAAGTAAGCCAGTGTGTGTTCCCATCTCTCCTAGCCGCCGCTG 3'TAAATCTTCATTCGGTCACACACACAAAGGTAGAGGATCGCGCGGAC	G 3' C 5'
L.46.16-12	5'ATTTTAGAAGTAAGCCAGTGTGTGTTCCCATCTCTCCTAGCCGCCGCTG 3'TAAATCTTCATTCGGTCACACACACAAAGGTAGAGGATCGCGCGGAC	G 3' C 5'
L.19.16-3	5'ATTTTAGAAGTAGGCTAGTGTGTGTTCCCATCTCTCCTAGCCGCCGCTG 3'TAAATCTTCATCCGATCACACACACAAAGGTAGAGGATCGCGCGGAC	G 3' C 5'
L.CEM/251	5'ATTTTAGAAGTAAGCTAGTGTGTGTTCCCATCTCTCCTAGCCGCCGCTG 3'TAAATCTTCATTCGATCACACACACAAAGGTAGAGGATCGCGCGGAC	G 3' C 5'
L.36.8-3	5'ATTTTAGAAGTAGGCTAGTGTGTGTTCCCATCTCTCCTAGCCGCCGCTG 3'TAAATCTTCATCCGATCACACACACAAAGGTAGAGGATCGCGCGGAC	G 3' C 5'

FIG. 49G

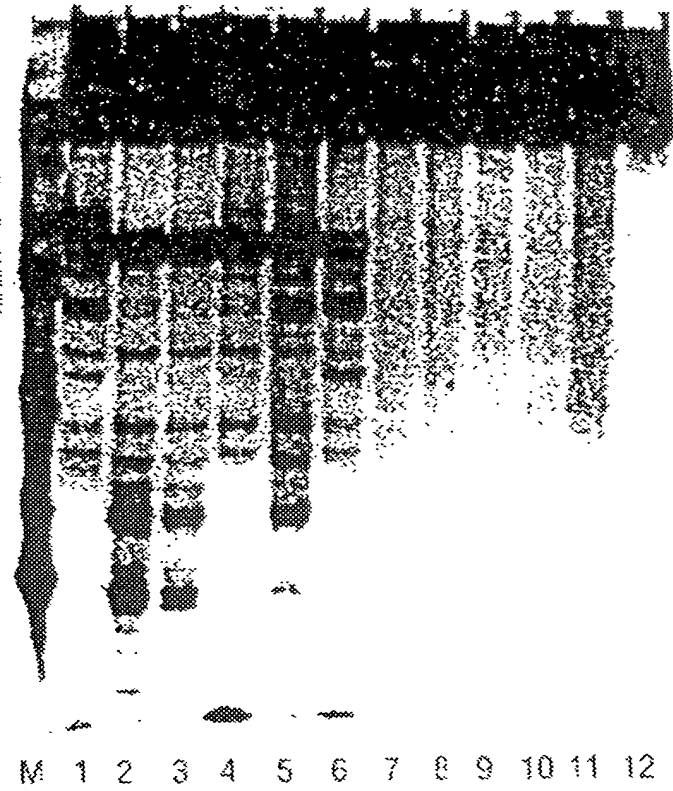


FIG. 50

M 1 2 3 4 5 6 7 8 9 10 11 12

FIG. 51

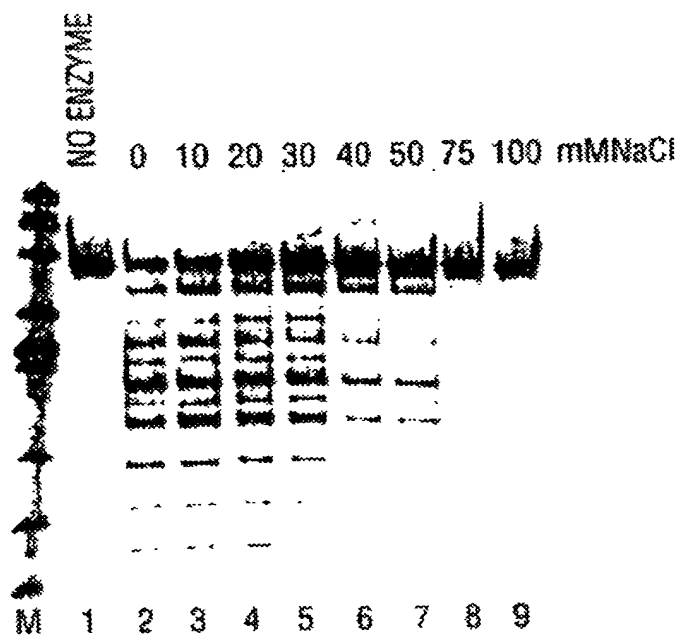


FIG. 52

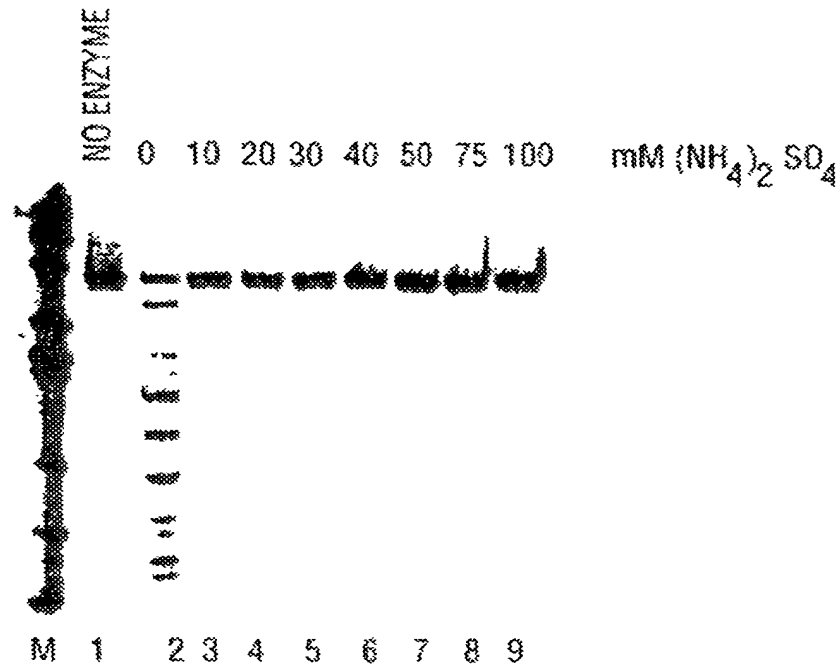


FIG. 53

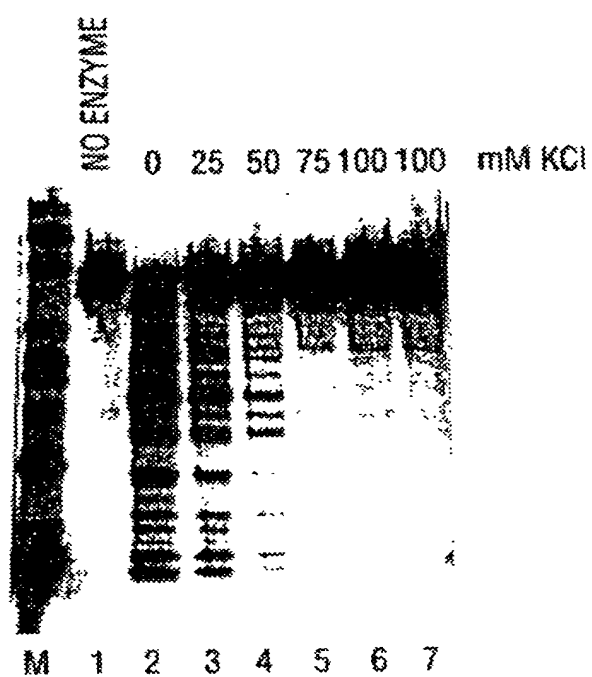


FIG. 54

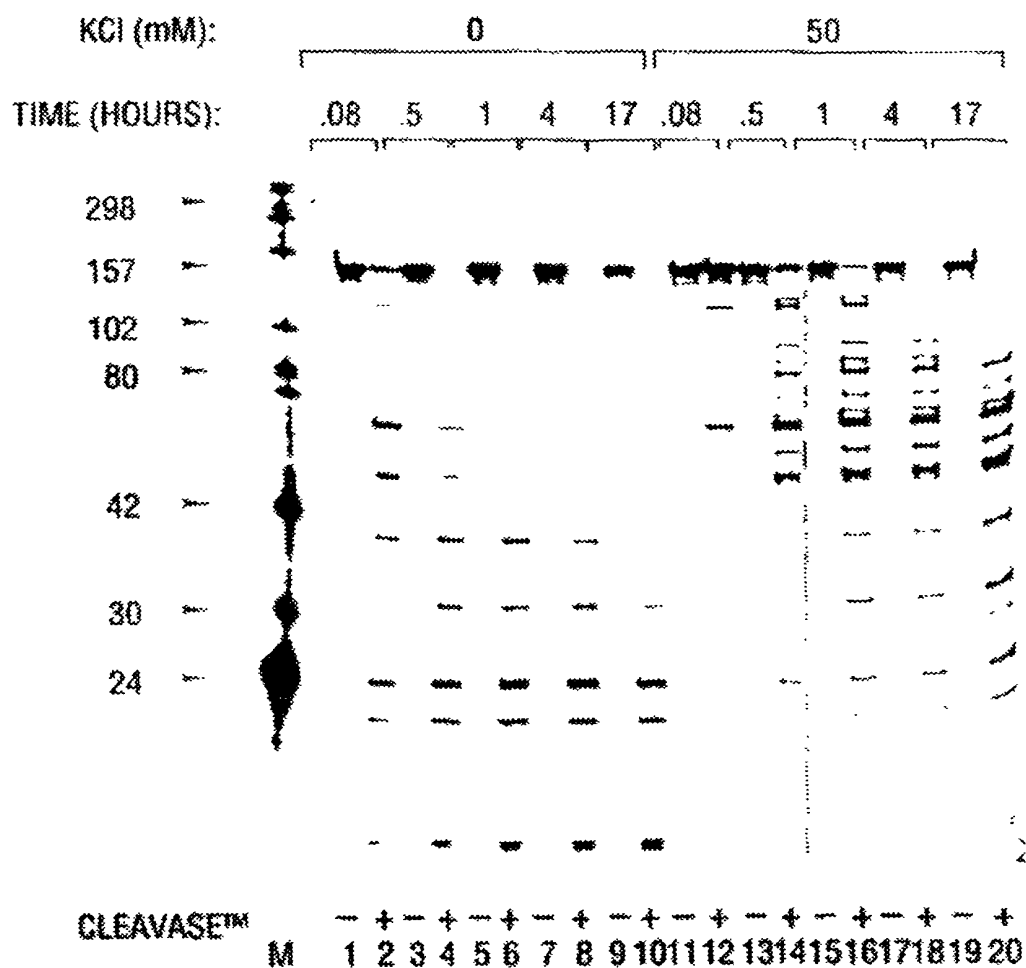


FIG. 55

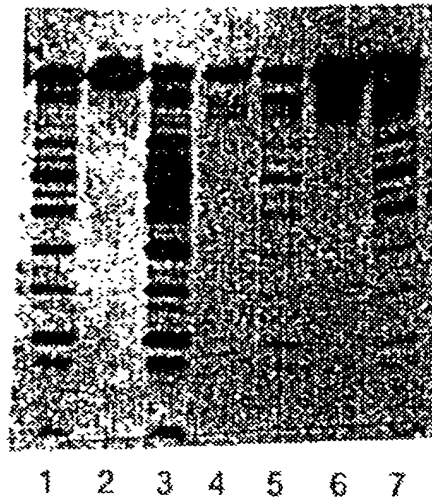


FIG. 56

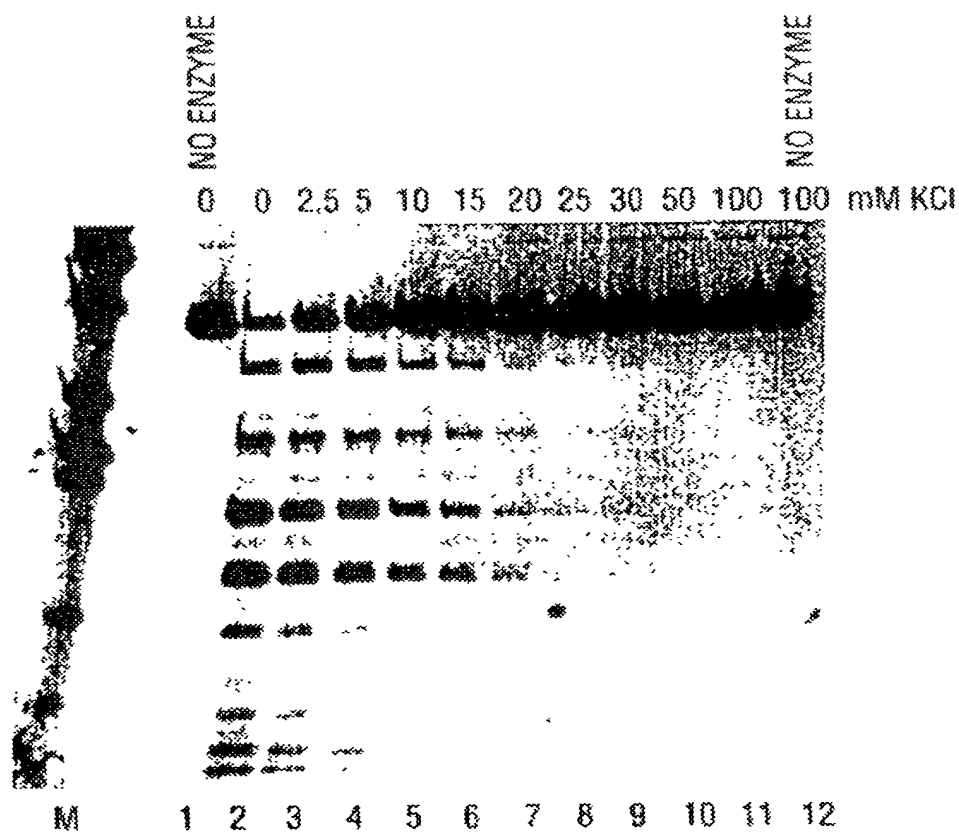


FIG. 57

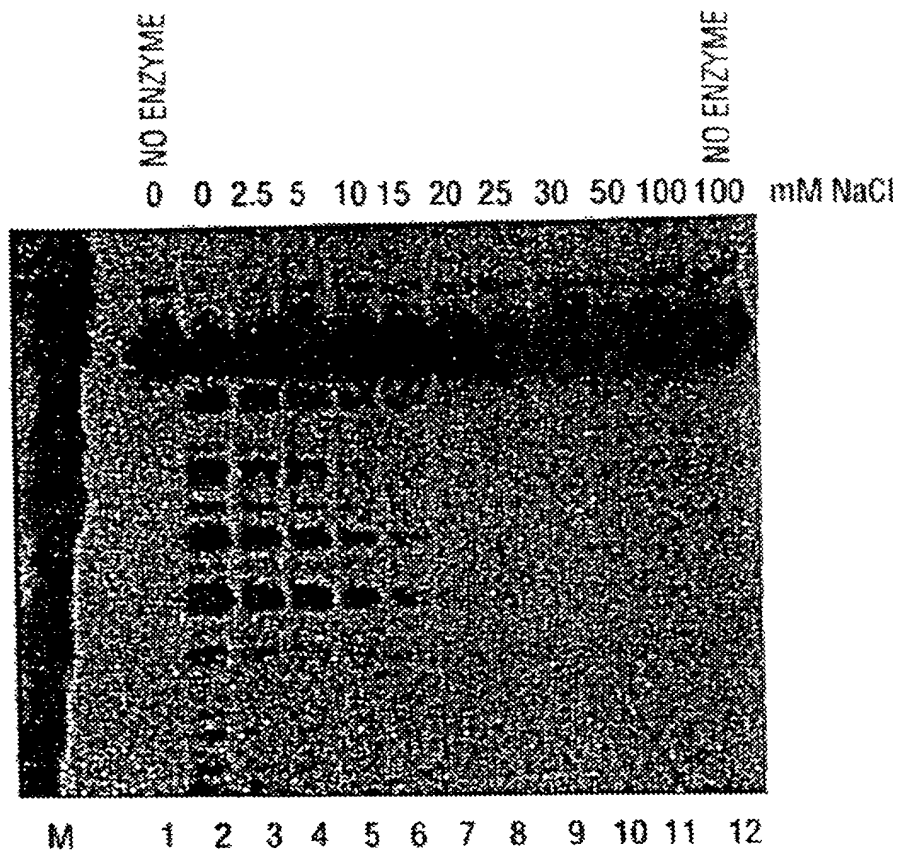


FIG. 58

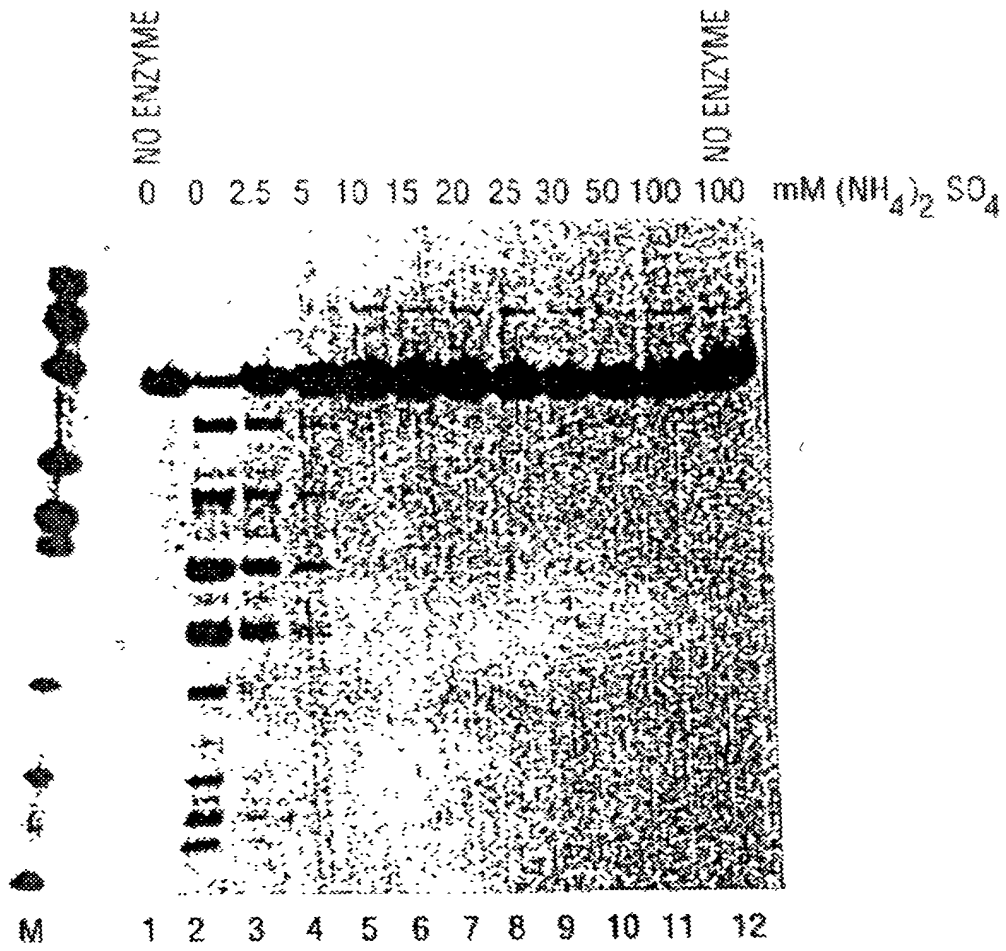


FIG. 59

TIME

0 5'' 1' 2' 5 10' 15' 20' 30' 1 HR 2 HR

1 2 3 4 5 6 7 8 9 10 11 12

NO ENZYME

FIG. 60

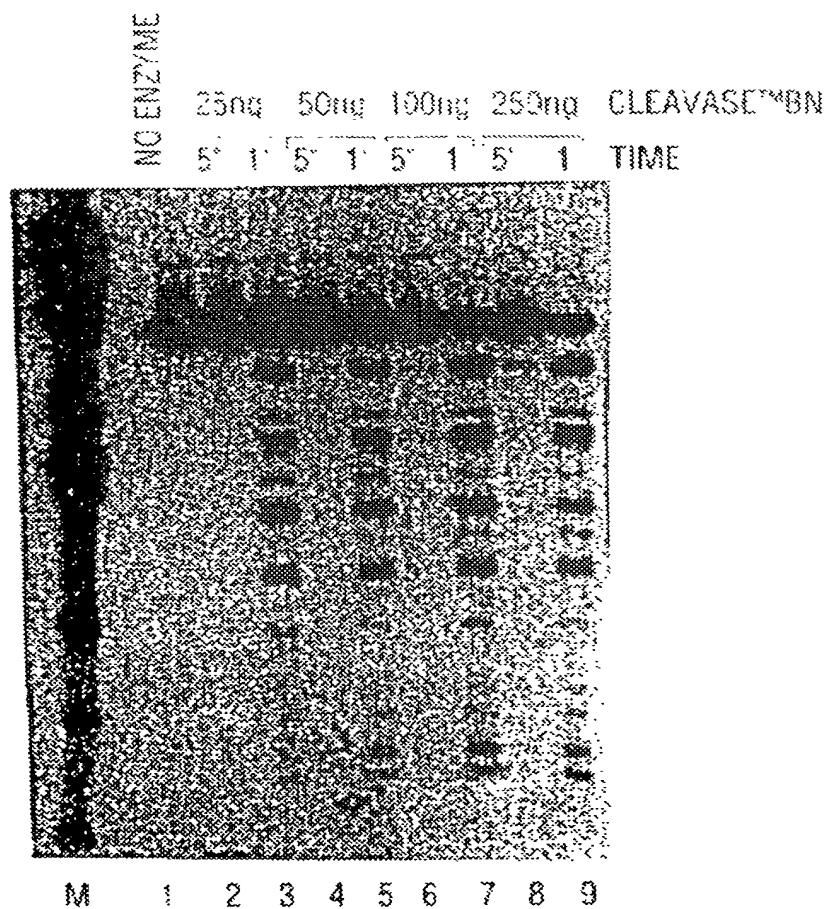


FIG. 61

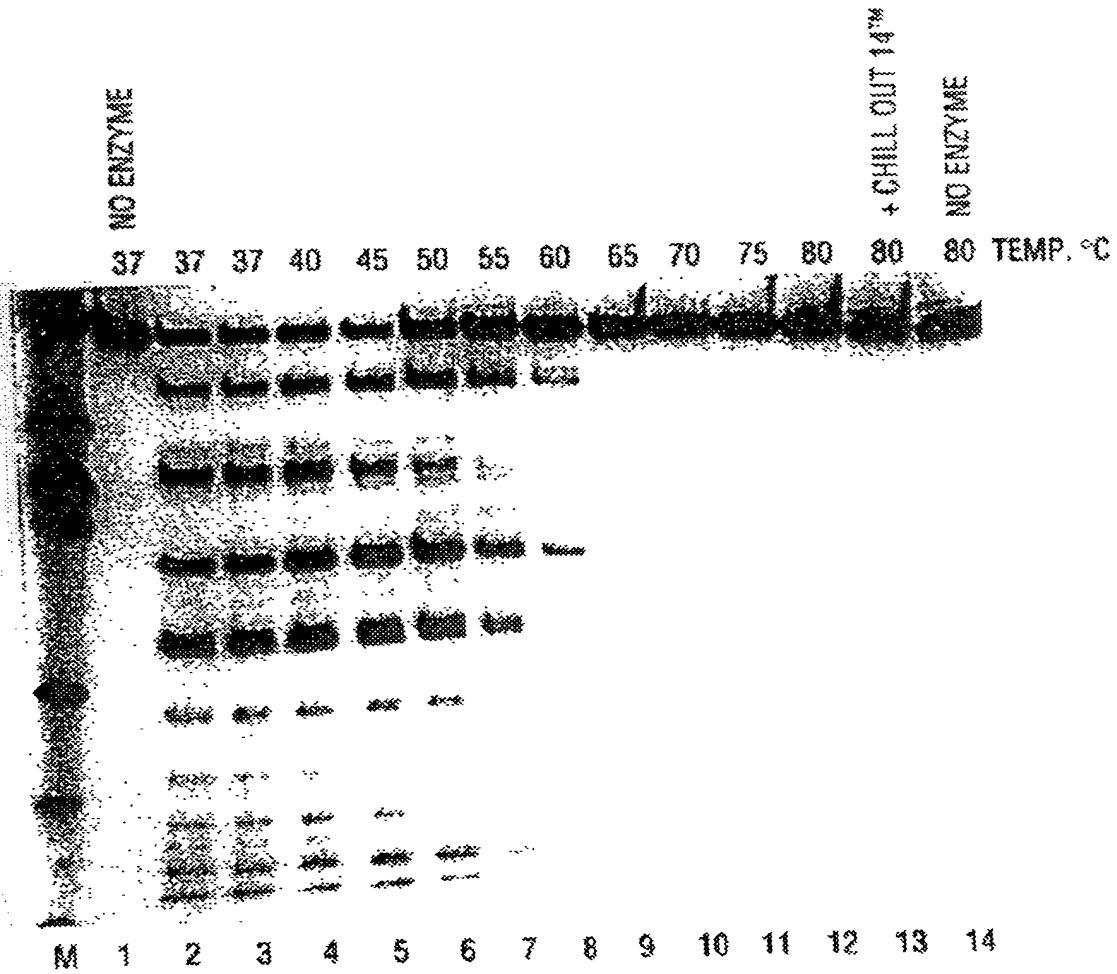


FIG. 62

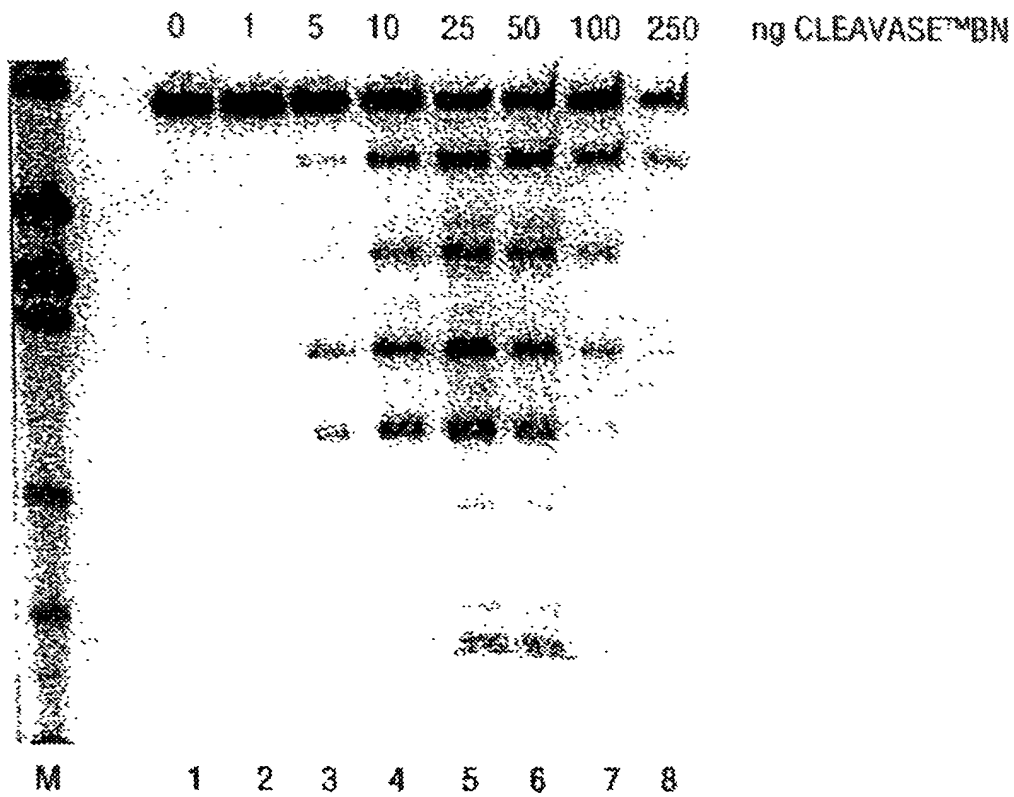


FIG. 63

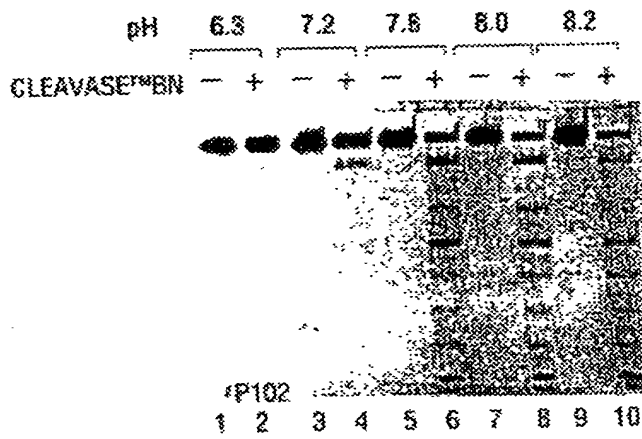


FIG. 64A

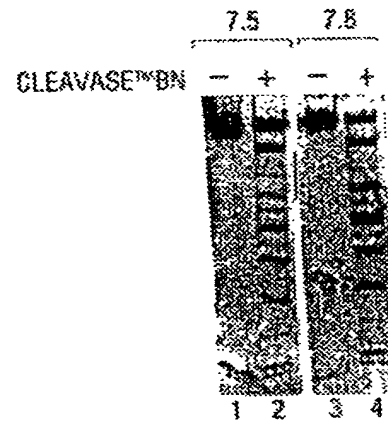


FIG. 64B

CLEAVASE™BN	pH 8.2		pH 7.2	
	+	-	+	-
<div style="display: flex; justify-content: space-around;"> 1 2 3 4 </div>				

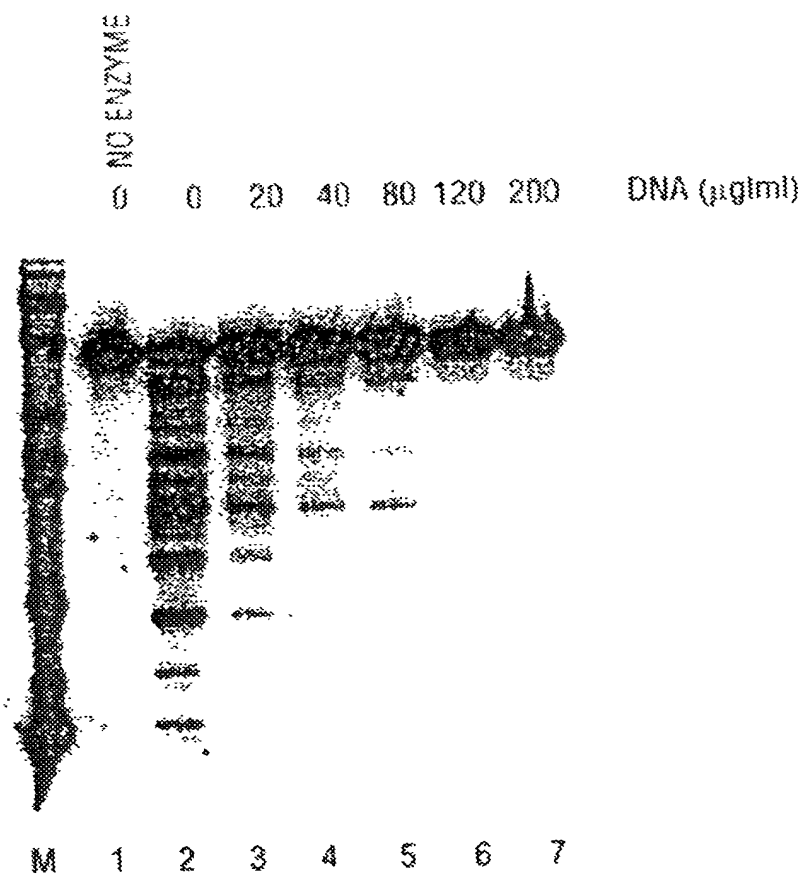


FIG. 66

NO ENZYME

5.0 1.25

0 50 0 50

UNITS TII DNAP

mM KCl

1 2 3 4 5

FIG. 67

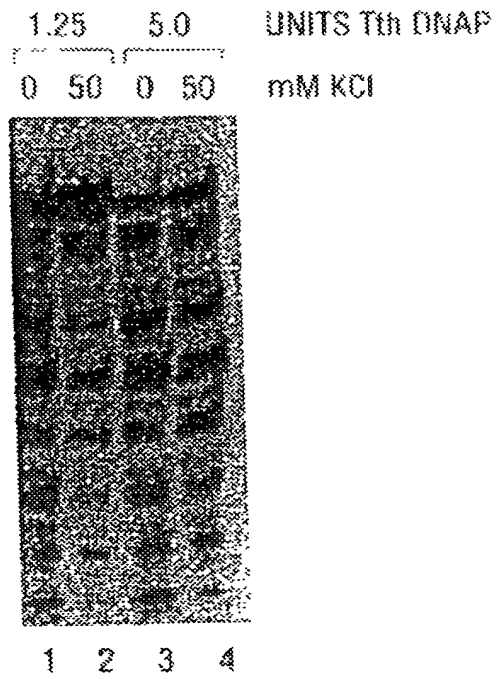


FIG. 68

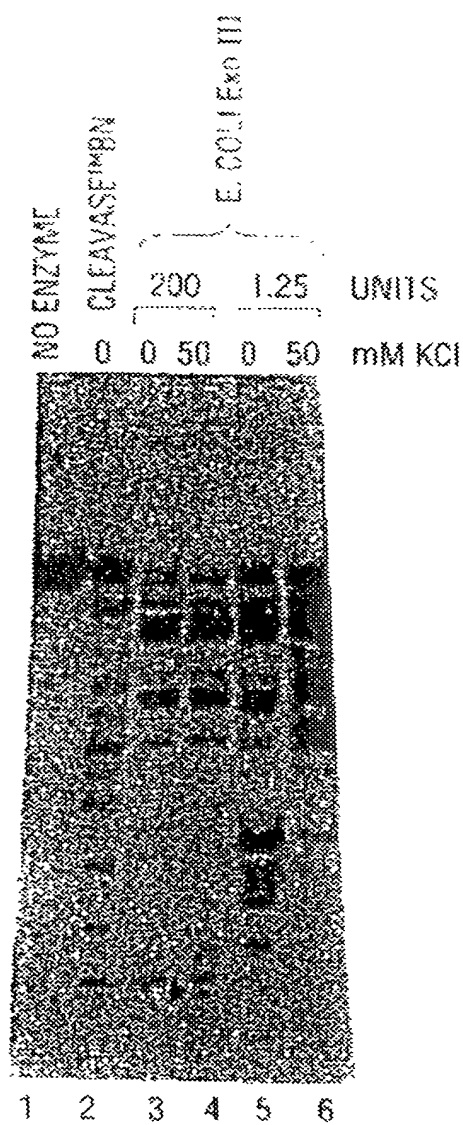


FIG. 69

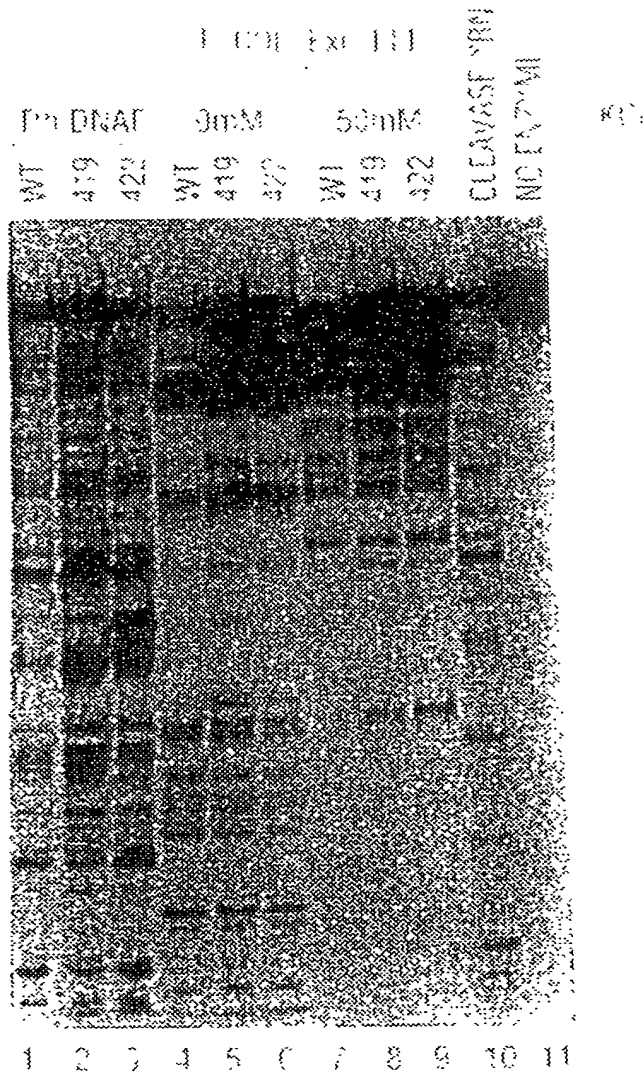
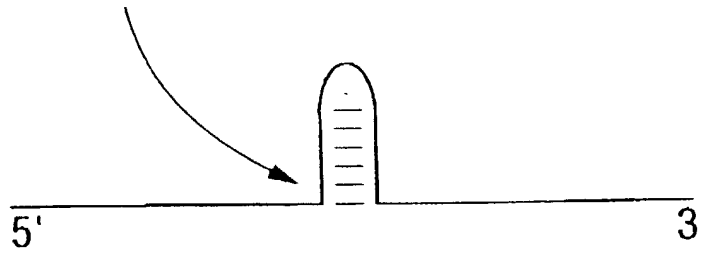


FIG. 70

5' CLEAVAGE SITE



3' CLEAVAGE SITE

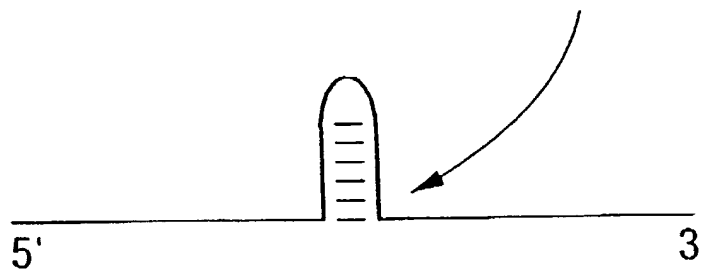


FIG. 71

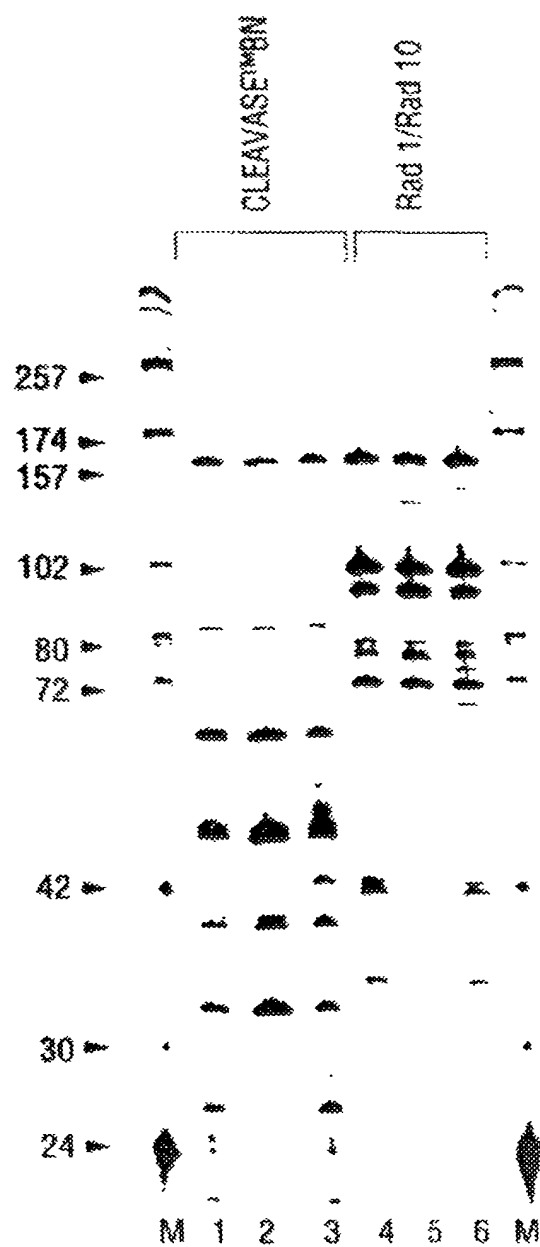
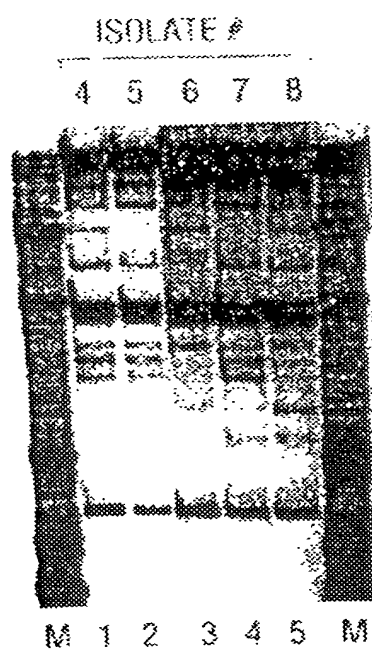
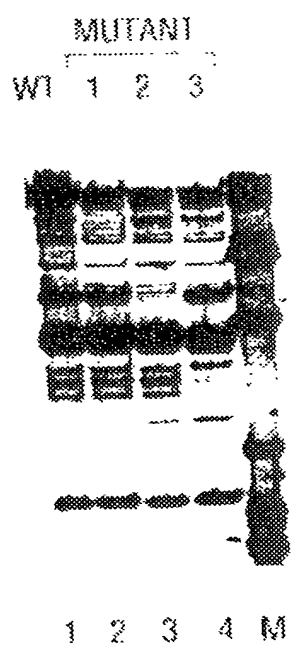


FIG. 72

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FIG. 73



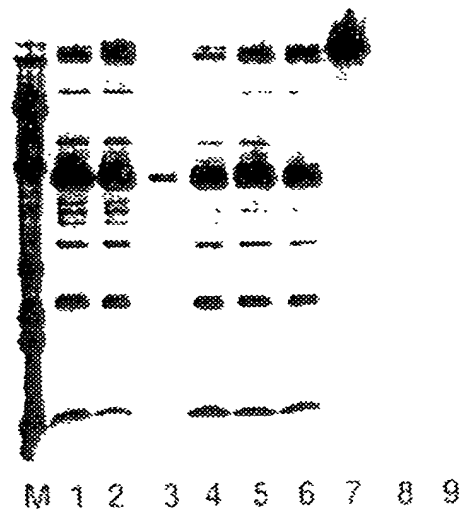


FIG. 75

% OF TOTAL
MUTATIONS

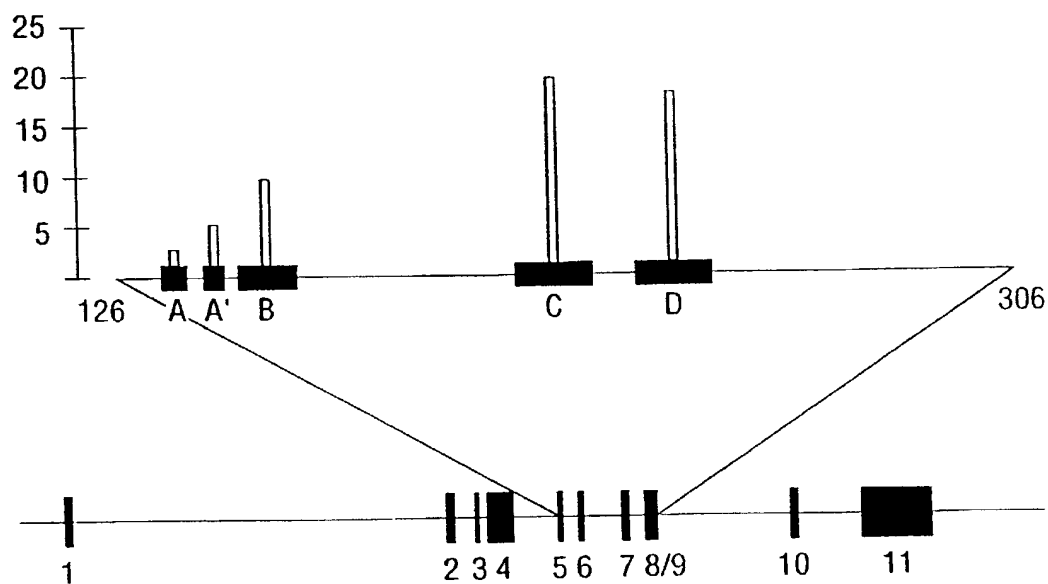


FIG. 76

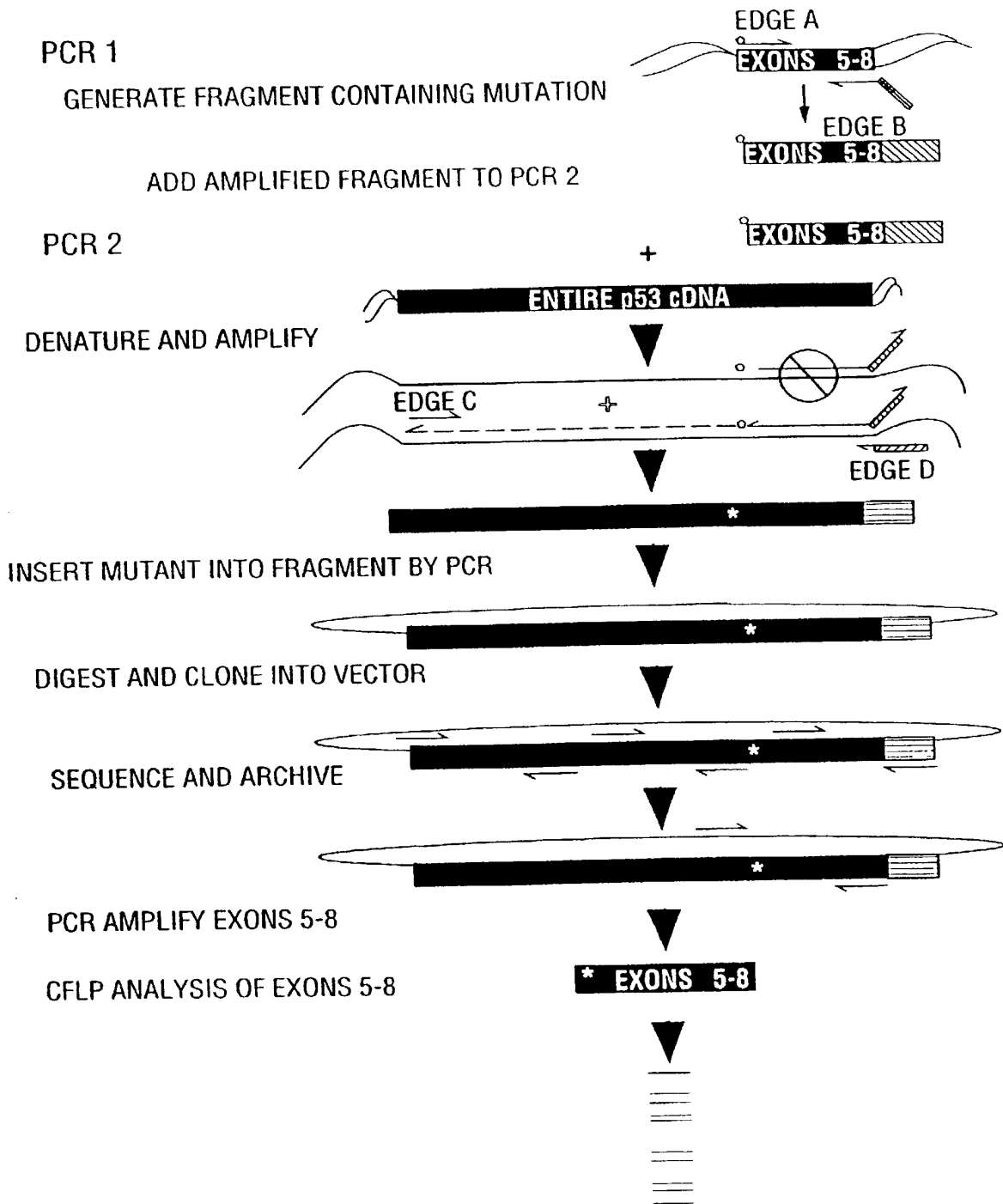


FIG. 77

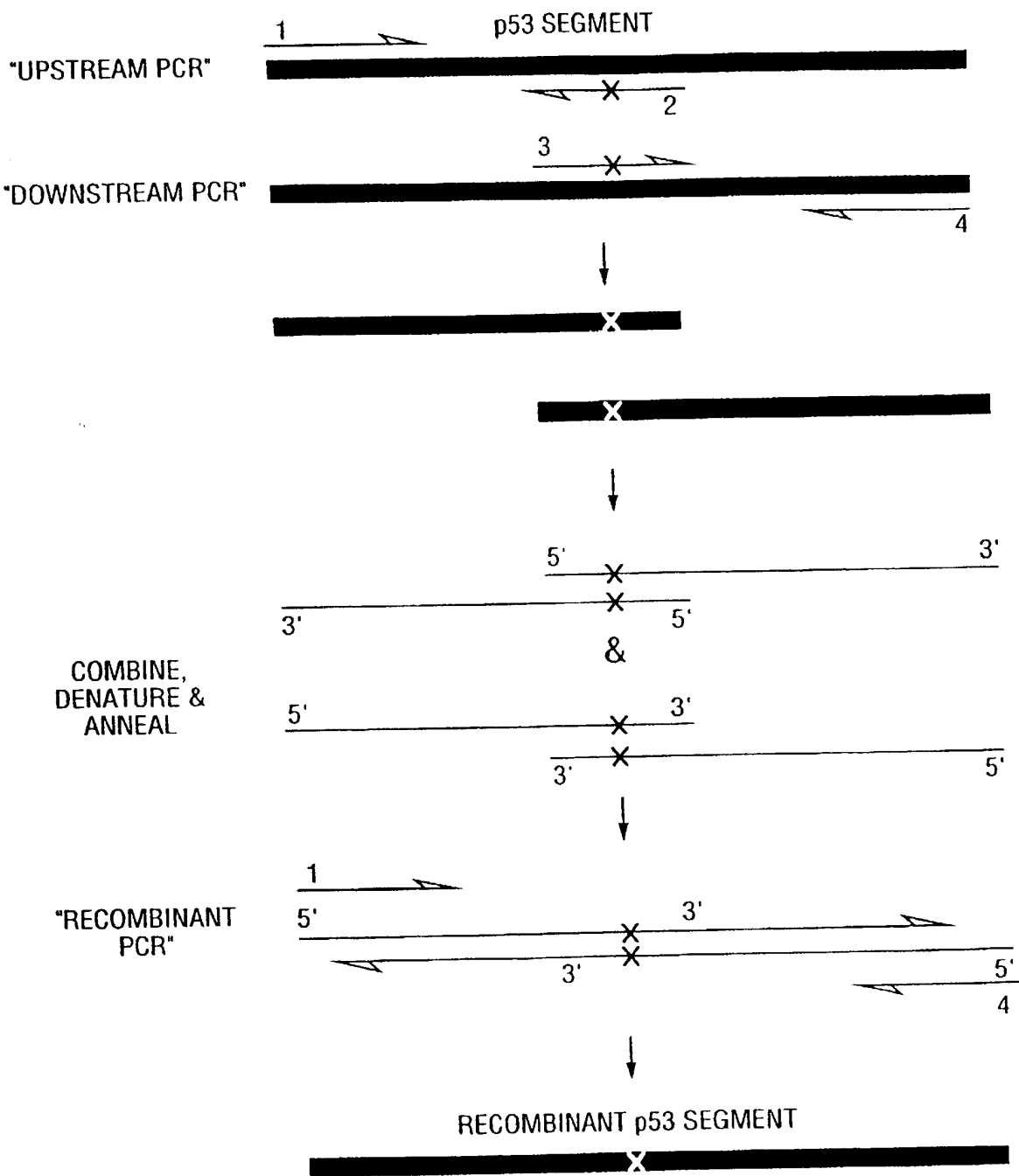


FIG. 78

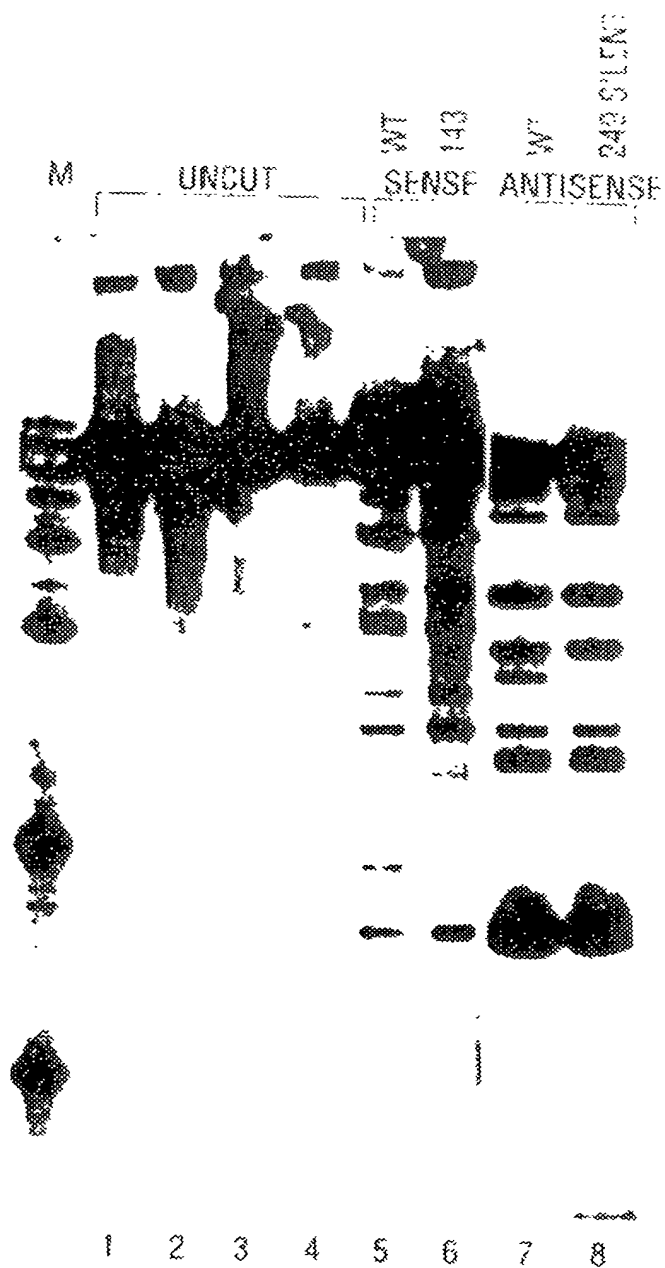


FIG. 79

WT 249 249 273 WT 249 249 273
R +S SILENT R +S SILENT

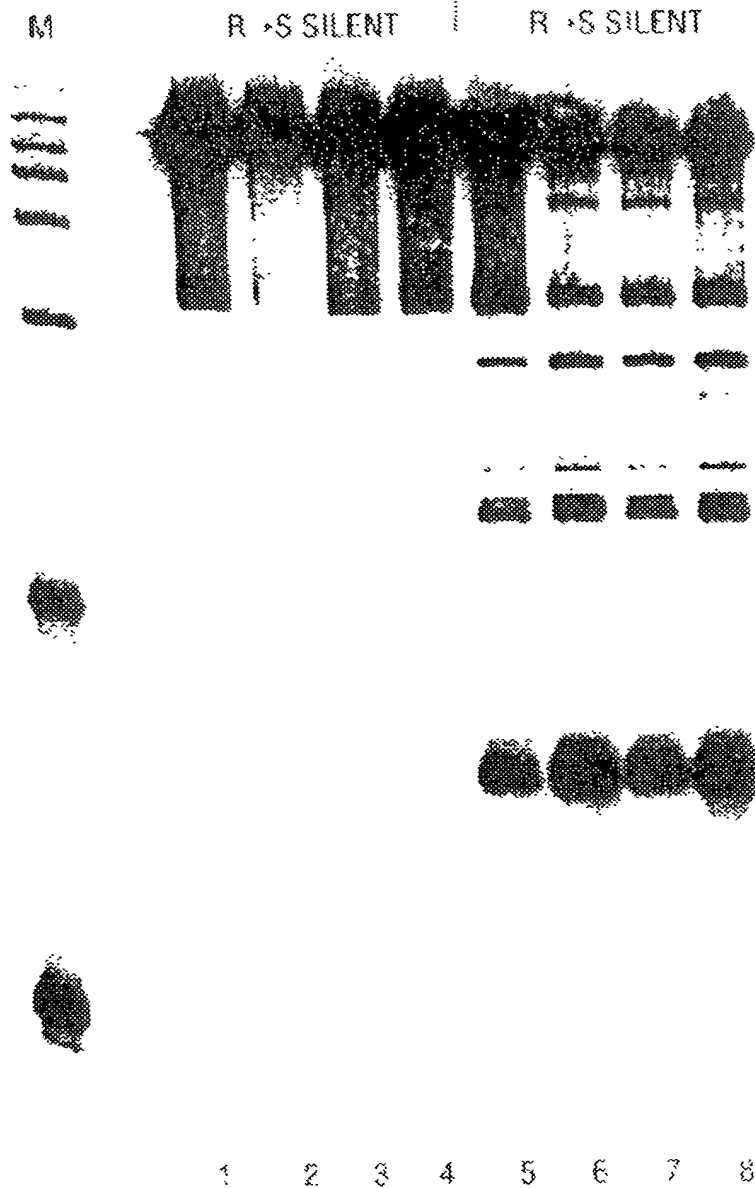


FIG. 80

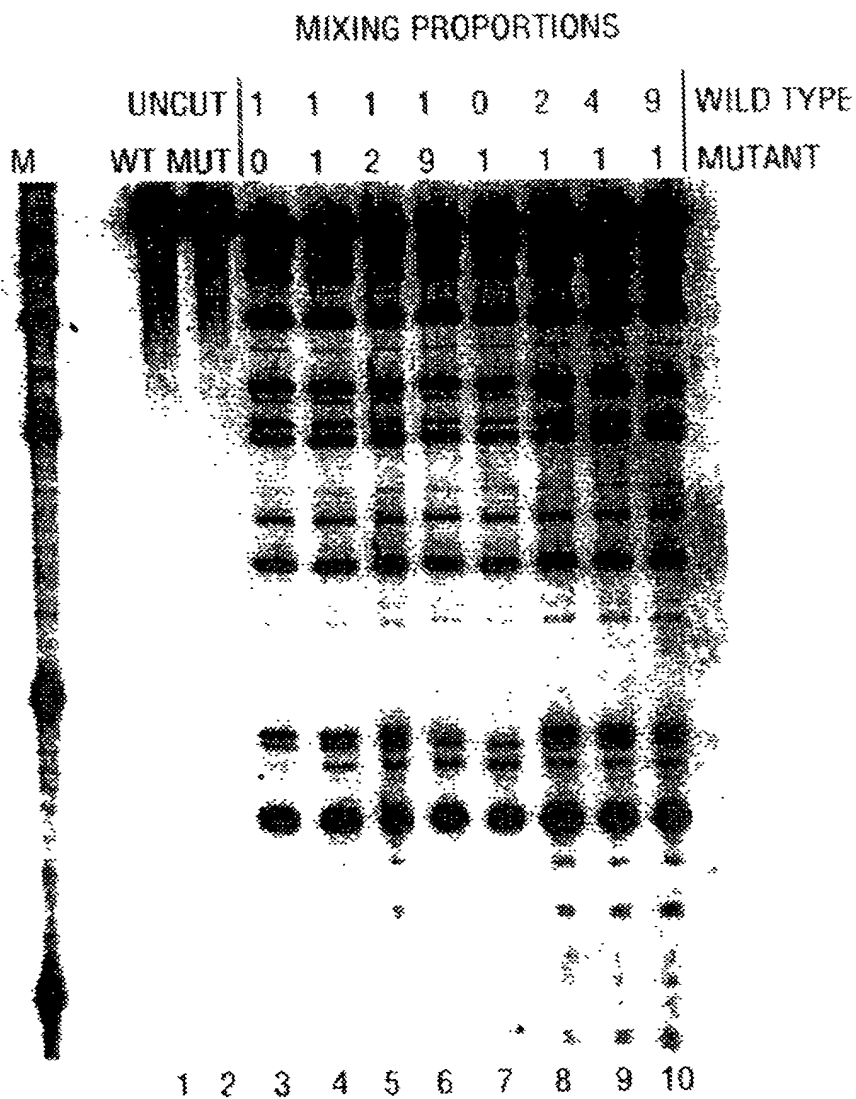


FIG. 81

HCV1.1	151	CCCGCTCAAT	GCCTGGAGAT	TTGGGCGTGC	CCCCGCAAGA	CTGCTAGCCG	200
HCV2.1		CCCGCTCAAT	GCCTGGAGAT	TTGGGCGTGC	CCCCGCAAGA	CTGCTAGCCG	
HCV3.1		CCCGCTCAAT	GCCTGGAGAT	TTGGGCGTGC	CCCCGCGAGA	CTGCTAGCCG	
HCV4.2		CCCGCTCAAT	GCCTGGAGAT	TTGGGCGTGC	CCCCGCAAGA	CTGCTAGCCG	
HCV6.1		CCCACTCIAT	GCCCGGCCAT	TTGGGCGTGC	CCCCGCAAGA	CTGCTAGCCG	
HCV7.1		CCCGCTCAAT	ACCCAGAAAT	TTGGGCGTGC	CCCCGCGAGA	ICACTAGCCG	
HCV1.1	201	AGTAGTGTG	GGTCGCGAAA	GGCCTTGTGG	TACTGCCCTGA	TAGGGTGCT	250
HCV2.1		AGTAGTGTG	GGTCGCGAAA	GGCCTTGTGG	TACTGCCCTGA	TAGGGTGCTT	
HCV3.1		AGTAGTGTG	GGTCGCGAAA	GGCCTTGTGG	TACTGCCCTGA	TAGGGTGCTT	
HCV4.2		AGTAGTGTG	GGTCGCGAAA	GGCCTTGTGG	TACTGCCCTGA	TAGGGTGCTT	
HCV6.1		AGTAGCGTTG	GGTIGCGAAA	GGCCTTGTGG	TACTGCCCTGA	TAGGGTGCTT	
HCV7.1		AGTAGTGTG	GGTCGCGAAA	GGCCTTGTGG	TACTGCCCTGA	TAGGGTGCTT	
HCV1.1	251	GCGAGTGCCC	CGGGAGGTCT	CGTAGACCGT	GC	282	
HCV2.1		GCGAGTGCCC	CGGGAGGTCT	CGTAGACCGT	GC		
HCV3.1		GCGAGTGCCC	CGGGAGGTCT	CGTAGACCGT	GC		
HCV4.2		GCGAGTGCCC	CGGGAGGTCT	CGTAGACCGT	GC		
HCV6.1		GCGAGTACCC	CGGGAGGTCT	CGTAGACCGT	GC		
HCV7.1		GCGAGTGCCC	CGGGAGGTCT	CGTAGACCGT	GC		

FIG. 82B

CGGAGGTCTCGTAGACCGTGC

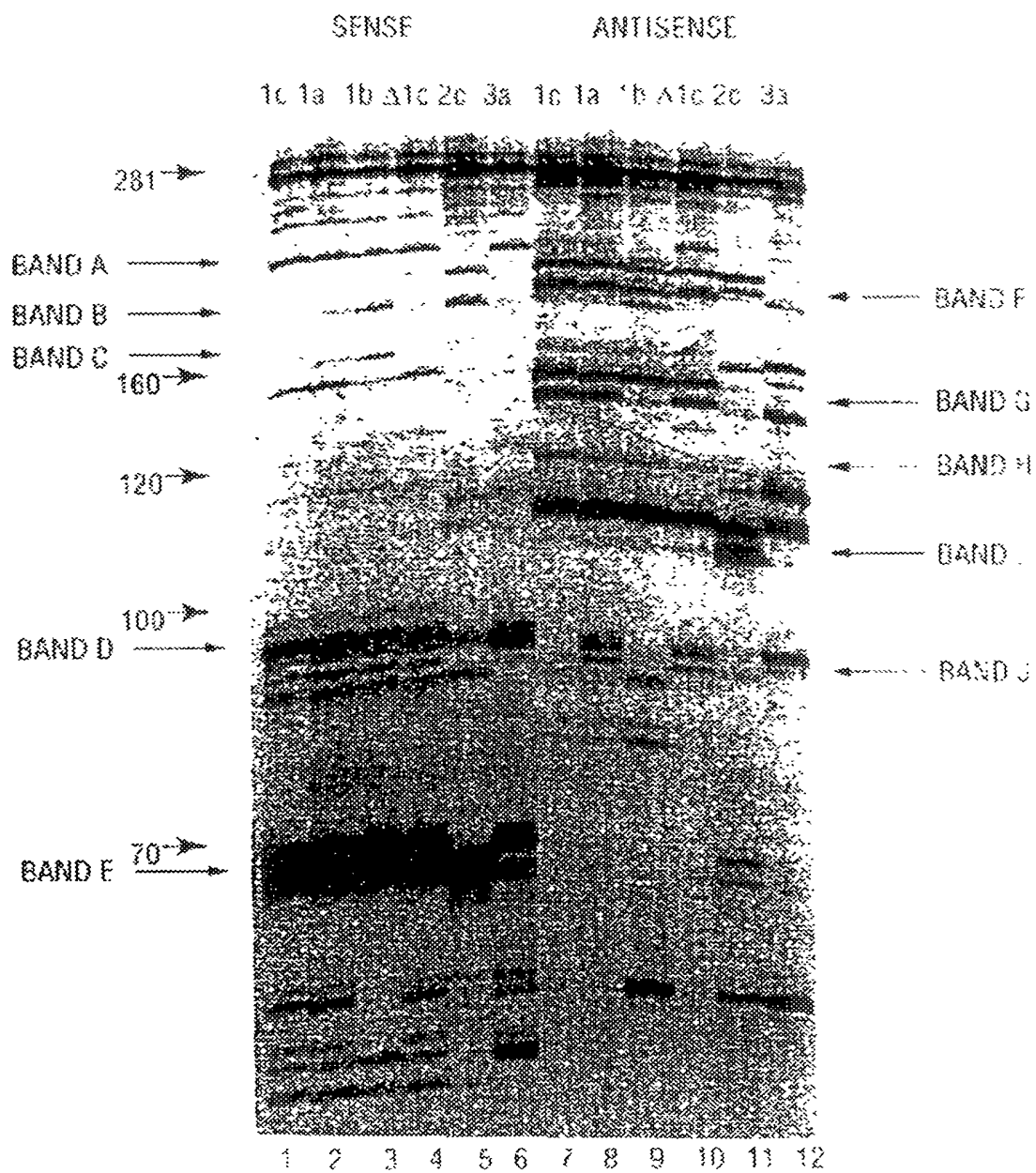


FIG. 83

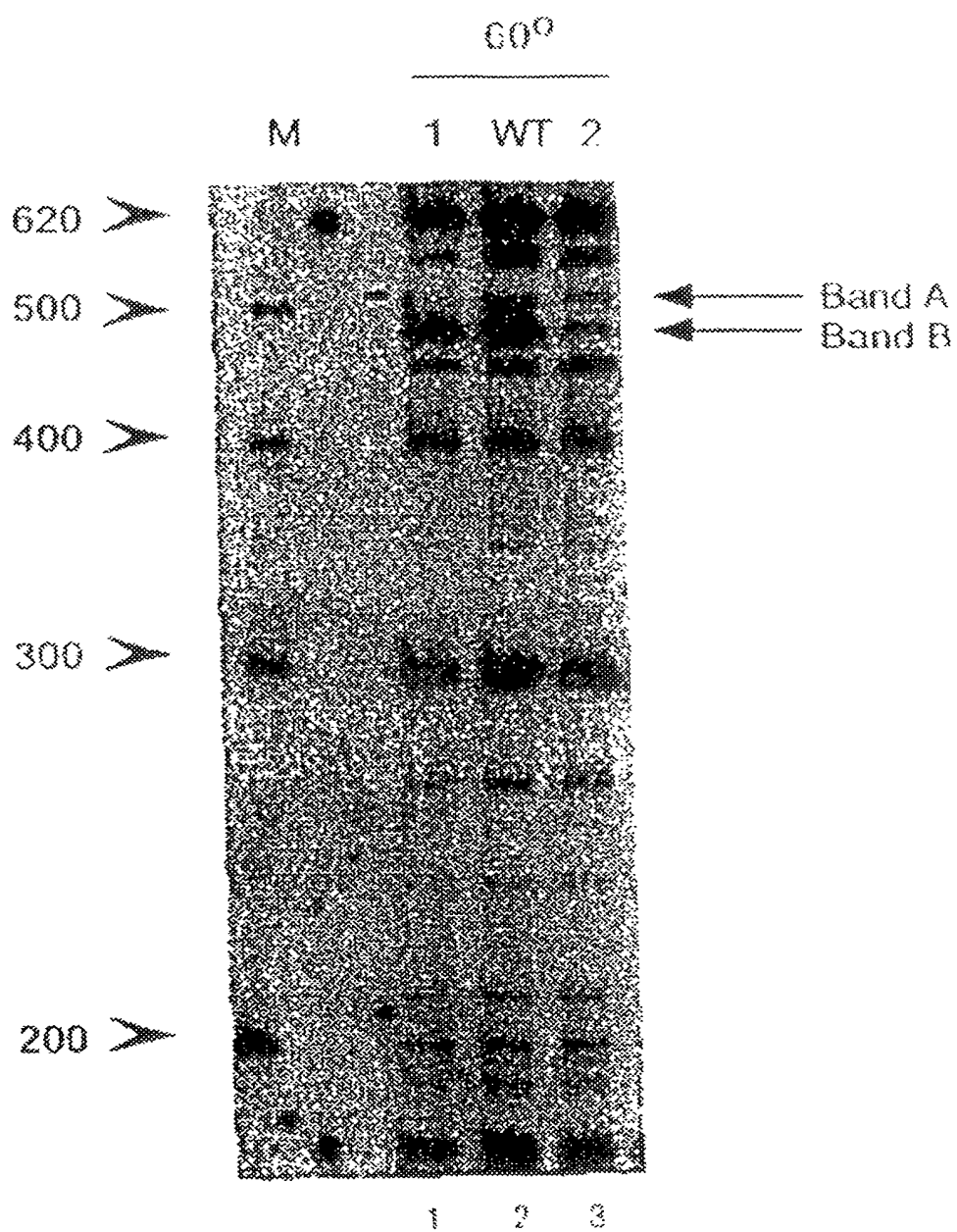


FIG. 84

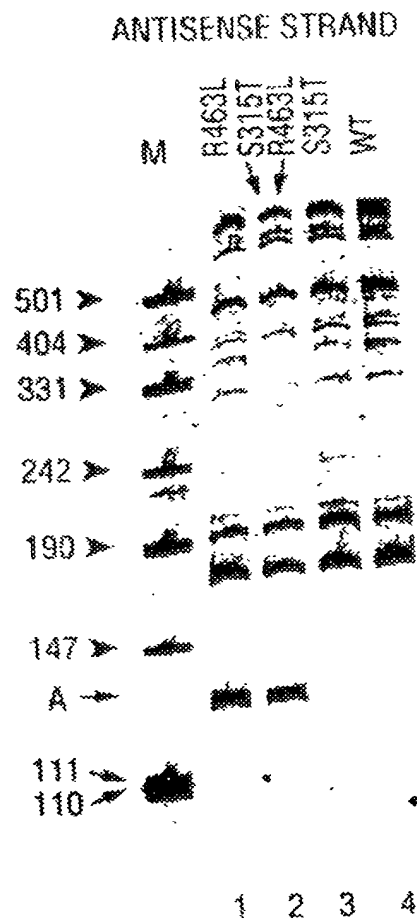


FIG. 87

10	20	30	40	50	60
AGA	GTTTGATCCT	GGCTCAG			
AAATTGAAGA	GTTTGATCAT	<u>GGCTCAGATT</u>	GAACGCTGGC	GGCAGGCCCTA	ACACATGCAA
TTTAACTTCT	CAAACCTAGTA	CCGAGTCTAA	CTTGCGACCG	CCGTCCGGAT	TGTGTACGTT
70	80	90	100	110	120
				GGCGGAC	GGGTGAGTAA
GTCGAACGGT	AACAGGAAGA	AGCTTGCTTC	TTTGCTGACG	<u>AGTGGCGGAC</u>	<u>GGGTGAGTAA</u>
CAGCTTGCCA	TTGTCTTCT	TCGAACGAAG	AAACGACTGC	TCACCGCCTG	CCCACCTCATT
130	140	150	160	170	180
TGTCTGGGAA	ACTGCCTGAT	GGAGGGGGAT	AACTACTGGA	AACGGTAGCT	AATACCGCAT
ACAGACCCCTT	TGACGGACTA	CCTCCCCCTA	TTGATGACCT	TTGCCATCGA	TTATGGCGTA
190	200	210	220	230	240
AACGTCGCAA	GACCAAAGAG	GGGGACCTTC	GGGCCTCTTG	CCATCGGATG	TGCCCCAGATG
TTGCAGCGTT	CTGGTTTCTC	CCCCTGGAAG	CCCGGAGAAC	GGTAGCCTAC	ACGGGTCTAC
250	260	270	280	290	300
GGATTAGCTA	GTAGGTGGG	TAACGGCTCA	CCTAGGCGAC	GATCCCTAGC	TGGTCTGAGA
CCTAATCGAT	CATCCACCCC	ATTGCCGAGT	GGATCCGCTG	CTAGGGATCG	ACCAGACTCT
310	320	330	340	350	360
GGATGACCCAG	CCACACTGGA	ACTGAGACAC	GGTCCAGACT	CCTACGGGAG	GCAGCAGTGG
CCTACTGGTC	GGTGTGACCT	TGACTCTGTG	<u>CCAGGTCIGA</u>	<u>GGATGCCCTC</u>	<u>CGTCGTCACC</u>
			TGA	GGATGCCCTC	CGTCGTC

FIG. 88A

370	380	390	400	410	420
GGAATATTGC	ACAATGGGCG	CAAGCCCTGAT	GCAGCCCATGC	CGCGTGTATG	AAGAAGGCCT
CCTTATAACG	TGTTACCCGC	GTTCCGACTA	CGTCGGTACG	CGGCACATAC	TTCTTCCGGA
430	440	450	460	470	480
TCGGGTTGTA	AAGTACTTTC	AGCGGGGAGG	AAGGGAGTAA	AGTTAATACC	TTTGCTCATT
AGCCCAACAT	TTCATGAAAG	TCGCCCCCTCC	TTCCCTCATT	TCAATTATGG	AAACGAGTAA
490	500	510	520	530	540
GACGTTACCC	GCAGAAGAAG	CACCGGCTAA	CTCCGTGCCA	GCAGCCGCGG	TAATACGGAG
CTGCAATGGG	CGTCTTCTTC	GTGGCCGATT	GAGGCACGGT	CGTCGGCGCC	ATTATGCCTC
550	560	570	580	590	600
GGTGCAAGCG	TTAATCGGAA	TTACTGGGCG	TAAAGCGCAC	GCAGGCGGTT	TGTTAAGTCA
CCACGTTTCG	AATTAGCCTT	AATGACCCGC	ATTTCCGGTG	CGTCCGCCAA	ACAATTTCAGT
610	620	630	640	650	660
GATGTGAAAT	CCCCGGGCTC	AACCTGGGAA	CTGCATCTGA	TACTGGCAAG	CTTGAGTCTC
CTACACTTTA	GGGGCCCGAG	TTGGACCCTT	GACGTAGACT	ATGACCGTTC	GAACTCAGAG
670	680	690	700	710	720
GTAGAGGGGG	GTAGAAATTCC	AGGTGTAGCG	GTGAAATGCG	TAGAGATCTC	GAGGAATACC
CATCTCCCCC	CATCTTAAGG	TCCACATCGC	CACTTTACGC	ATCTCTAGAC	CTCCTTATGG
730	740	750	760	770	780
GGTGGCGAAG	GCGGCCCCCT	GGACGAAGAC	TGACGCTCAG	GTGCGAAAGC	GTGGGGAGCA
CCACCGCTTC	CGCCGGGGGA	CCTGCTTCTG	ACTGCGAGTC	CACGCTTTTCG	CACCCCTCGT

FIG. 88B

400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780

1210	1220	1230	1240	1250	1260
ATCATGGCCC	TTA				
ATCATGGCCC	TTACGA				
ATCATGGCCC	TTACGACCAG	GGCTACACAC	GTGCTACAAT	GGCGCATACA	AAGAGAAGCG
TAGTACCGGG	AATGCTGGTC	CCGATGTGTG	CACGATGTTA	CCGCGTATGT	TTCTCTTCGC
1270	1280	1290	1300	1310	1320
ACCTCGCGAG	AGCAAGCGGA	CCTCATAAAG	TGCGTCGTAG	TCCGGATTGG	AGTCTGCAAC
TGGAGCGCTC	TCGTTGCCT	GGAGTATTTT	ACGCAGCATC	AGGCCTAACC	TCAGACGTTG
1330	1340	1350	1360	1370	1380
TCGACTCCAT	GAAGTCGGAA	TCGCTAGTAA	TCGTGGATCA	GAATGCCACG	GTGAATACGT
AGCTGAGGTA	CTTCAGCCTT	AGCGATCAAT	AGCACCTAGT	CTTACGGTGC	<u>CACCTTATGCA</u>
				GC	CACTTATGCA
1390	1400	1410	1420	1430	1440
TCCCCGGCCT	TGTACACACC	GCCCCGTCACA	CCATGGGAGT	GGGTTGCAAA	AGAAAGTAGGT
<u>AGGGCCCCGA</u>	<u>ACATGTGTGG</u>	CGGGCAGTGT	GGTACCCCTCA	CCCAACGTTT	TCTTCATCCA
AGGGCCCCGA	ACATG				
1450	1460	1470	1480	1490	1500
AGCTTAACCT	TCGGGAGGGC	GCTTACCACCT	TTGTGATTCA	TGACTGGGGT	GAAGTCGTAA
TCGAAATTGA	AGCCCTCCCG	CGAATGGTGA	AACACTAAGT	ACTGACCCCA	CTTCAGCATT
1510	1520	1530	1540	1550	
CAAGGTAACC	GTAGGGGAAC	CTGCGGTTGG	ATCACCTCCT	TA.....	
GTTCCATTGG	CATCCCCTTG	GACGCCAAC	TAGTGGAGGA	AT.....	

FIG. 88D

```

1638 (SEQ ID NO:151)          AGAGTTTGATCCTGGCTCAG
E.colirrse (SEQ ID NO:158) 0 ...AAATTGAAGAGTTTGATCATGGCTCAGATTGAACGCTGGCGGCAGGCCCTAACACATGCA
Cam.jejun5 (SEQ ID NO:159) 0 ~TTTTATGGAGAGTTTGATCCCTGGCTCAGAGTGAACGCTGGCGCGTGCCTAATACATGCA
Stp.aureus (SEQ ID NO:160) 0 ..TTTTATGGAGAGTTTGATCCCTGGCTCAGGATGAACGCTGGCGCGTGCCTAATACATGCA

ER10 (SEQ ID NO:152)
E.colirrse
Cam.jejun5
Stp.aureus
60 AGTCGAACGGTAACAG----GAAGAAGCTTGCTTCTTT----GCTGACGAGTGGCGGACGGG
62 AGTCGAACGAT-----GAAGCTTCTAGCTTGCTAGAAGTGA-----TTAGTGGCGCACGGG
61 AGTCGAGCGAA-----CGGACGAGAAGCTTGCTTCTCTGATG----TT-AGCGGCGGACGGG
GGCGGACGGG

TGAGTAA
114 TGAGTAATGTCTGGGA-AACTGCCTGATGGAGGGGATAAATACTGGAACGGTAGCTAATA
114 TGAGTAAGGTATAGTTAATCTGCCCTACACAAGAGGACAACAGTTGGAAACGACTGCTAATA
113 TGAGTAACACGCTGGATAACCTACCTAAGACTGGGATAAATTTCGGGAACCGGAGCTAATA

175 CCGCATAAC-----GTCGCAAGAC-----CAAAGAGGGGACCTTTCG-GGCCTCTTG
176 CTCTATACTCCTGCTTAACACAAGTTGAGTAGG-GAAAG-----TTTTT-----CG
175 CCGGATAATATTTTGAACCGCATGGTTCAAAAGTGAAAGACGGT----CTT----GCTGTCA

221 CCATCGGATGTGCCCAGATGGGATTAGCTAGTGGGTAAACGGCTCACCTAGGCGACGA
221 GTGTAGGATGAGACTATATAGTATCAGCTAGTTGGTAAGGTAATGGCTTACCAAGGCTATGA
229 CTTATAGATGGATCCGCGCTGCATTAGCTAGTTGGTAAGGTAAACGGCTTACCAAGGCAACGA

283 TCCCTAGCTGGTCTGAGAGGATGACCAGCCACACTGGAACGTGAGACACGGTCCAGACTCCCTA
283 CGCTTAACCTGGTCTGAGAGGATGATCAGTCACACTGGAACGTGAGACACGGTCCAGACTCCCTA
291 TACGTAGCCGACCTGAGAGGGTGTATCGGCCACACTGGAACGTGAGACACGGTCCAGACTCCCTA
ACTCCTA

```

FIG. 89A

FIG. 89A

E.colirrsE
Cam.jejun5
Stp.aureus
1659 (COMPL)

345 CGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGCAAGCCTGATGCAGCCATGCCGCGTG
345 CGGGAGGCAGCAGTAGGGAATATTGCGCAATGGGGAAACCCCTGACGCAGCAACGCCGCGTG
353 CGGGAGGCAGCAGTAGGGAATCTTCCGCAATGGGCGAAAGCCTGACGGAGCAACGCCGCGTG
CGGGAGGCAGCAG

E.colirrsE
Cam.jejun5
Stp.aureus

407 TATGAAGAAGGCCTTCGGGTTGTAAAGTACTTTTCAGCGGGGAGGAA-GGGAGTAAAGTTAAT
407 GAGGATGACACTTTTCGGAGCGTAAACTCCTTTTCTTAGGGAAG -----AATT
415 AGTGATGAAGGTCTTCGGATCGTAAACTCTGTTATTAGGGAAGAACATATGTGTAAGTAAC

E.colirrsE
Cam.jejun5
Stp.aureus

468 ACCTTTGCTCATTGACGTTACCCGCAGAAGAAGCACCCGGCTAACTCCGTGCCAGCAGCCGCG
455 C-----TGACGGTACCTAAGGAATAAGCACCGGCTAACTCCGTGCCAGCAGCCGCG
476 -TGTGCACATCTTGACGGTACCTAATCAGAAAGCCACGGCTAACTACGTGCCAGCAGCCGCG

FIG. 89B

FIG. 89B

E.colirrsE	530	GTAATACGGAGGGTGCAAGCGTTAATCGGAATTACTGGCGTAAAGCGCACGCAGGCGGTTT
Cam.jejun5	506	GTAATACGGAGGGTGCAAGCGTTAATCGGAATCACTGGCGTAAAGGCGCGTAGGCGGATT
Stp.aureus	538	GTAATACGTAGGTGGCAAGCGTTATCCGGAATTATTGGGCGTAAAGCGCGCGTAGGCGGTTT
E.colirrsE	592	GTTAAGTCAGATGTGAAATCCCCGGGCTCAACCTGGGAACTGCATCTGATACTGGCAAGCTT
Cam.jejun5	568	ATCAAGTCTCTTGTGAAATCTAATGGCTTAACCATTAACCTGCTTGGGAACTGATAGTCTA
Stp.aureus	600	TTTAAGTCTGATGTGAAAGCCACGGCTCAACCGTGGAGGCTCATTGGAACTGGAAACTT
E.colirrsE	654	GAGTCTCGTAGAGGGGGGTAGAAATCCAGGTGTAGCGGTGAAATGCGTAGAGATCTGGAGGA
Cam.jejun5	630	GAGTGAGGGAGAGGCAGATGGAAATTGGTGGTGTAGGGGTAAATCCGTAGATATCACCAAGA
Stp.aureus	662	GAGTGCAGAAAGAGGAAAGTGGAAATCCATGTGTAGCGGTGAAATGCCAGAGATATGGAGGA
E.colirrsE	716	ATACCGGTGGCGAAGGGCGGCCCTGGACGAAGACTGACGCTCAGGTGCCGAAAGCGTGGGGA
Cam.jejun5	692	ATACCCATTGCGAAGGCGATCTGCTGGAACTCAACTGACGCTAAGGCGCGAAAGCGTGGGGA
Stp.aureus	724	ACACCACTGGCGAAGGCGACTTCTGTGCTGTAACTGACGCTGATGTGCCGAAAGCGTGGGGA
E.colirrsE	778	GCAAACAGGATTAGATACCCCTGGTAGTCCACGCCGTAAACGATGTCGACTTGGAGGTTGTGC
Cam.jejun5	754	GCAAACAGGATTAGATACCCCTGGTAGTCCACGCCCTAAACGATGTACACTAGTTGTTGGGGT
Stp.aureus	786	TCAAACAGGATTAGATACCCCTGGTAGTCCACGCCGTAAACGATGAGTGCTAAGTGTTAGGGG

FIG. 89C

<i>E.colirrsE</i>	840	C-CTTGA-GGCGTGGCTTCCGGAGCTAACGCGTTAAGTCGACCGCCTGGGGAGTACGGCCGC
<i>Cam.jejun5</i>	816	G-CTAGT-CATCTCAGTAATGCAGCTAACGCCATTAAAGTGTACCGCCTGGGGAGTACGGTCGC
<i>Stp.aureus</i>	848	GT-TTCCGCCCCCTTAGTGCTGCAGCTAACGCATTAAAGCACTCCGCCTGGGGAGTACGACCCG
<i>E.colirrsE</i>	900	AAGGTTAAACTCAAATGAATTGACGGGGGCCCGCACAAAGCGGTGGAGCATGTGTTTAATT
<i>Cam.jejun5</i>	876	AAGATTAAACTCAAAGGAATAGACGGGGACCCGCCACAAGCGGTGGAGCATGTGTTTAATT
<i>Stp.aureus</i>	909	AAGGTTGAACTCAAAGGAATTGACGGGGACCCGCCACAAGCGGTGGAGCATGTGTTTAATT
<i>E.colirrsE</i>	962	CGATGCAACGCCGAAGAACCTTACCTGGTCTTGACATCCACGGAAGTTTTTCAGAGATGAGAAT
<i>Cam.jejun5</i>	938	CGAAGATACGCCGAAGAACCTTACCTGGGCTTGATATCCTAAGAACCTTTTAGAGATAAGAGG
<i>Stp.aureus</i>	971	CGAAGCAACGCCGAAGAACCTTACCAAATCTTGACATCCTTTGACAACTCTAGAGATAGAGCC
<i>E.colirrsE</i>	1024	GTG--CCTTCGGG--AA-CCGTGAGACAGGTGCTGCATGGCTGTCGTGCTCAGCTCGTGTGTGA
<i>Cam.jejun5</i>	1000	GTGCTAGCTTGCTAGAA-CTTAGAGACAGGTGCTGCACGGCTGTCGTGCTCAGCTCGTGTGTGA
<i>Stp.aureus</i>	1033	TTCC-CCTTCGGG--GGACAAAGTGACAGGTGGTGCATGGTTGTCGTGCTCAGCTCGTGTGTGA
SB-1		GCAACGAGCGCAACCC
<i>E.colirrsE</i>	1081	AATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTATCCTTTGTTGCCAGCGGTCCGG-CC
<i>Cam.jejun5</i>	1061	GATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCACGTAATTTAGTTGCTAACGGTTCGG-CC
<i>Stp.aureus</i>	1092	GATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTAAGCTTAGTTGCCATCA-TTAAGT-T

FIG. 89D

SB-3 (SEQ ID NO:157)	ATGACGTC	AAGTTCATC
SB-4 (SEQ ID NO:154)	ATGACGTC	AAGTTCATC
E.colirrsE	1142	GGGAAC
Cam.jejun5	1122	GAGCACTCTAAATAGACTGCCTTCG-TAAGGAGGAGGAAGGTGTGGACGACGTCAAGTTCATC
Stp.aureus	1152	GGGCACTCTAAGTTGACTGCCGGTGACAAACCGGAGGAAGGTGGGATGACGTCAAATCATC
SB-3		ATGGCCCCCTTA
SB-4		ATGGCCCCCTTACGA
E.colirrsE	1204	ATGGCCCCCTTACGACACGGGTACACACGTGCTACAAATGGCGCATACAAAAGAGAGCGACCTC
Cam.jejun5	1183	ATGGCCCCCTTATGCCACGGCGACACACGTGCTACAAATGGCATATAGAAATGAGACGCAATACCTC
Stp.aureus	1214	ATGGCCCCCTTATGATTTGGGCTACACACGTGCTACAAATGGACAATACAAAGGGCAGCGAAACCTC
E.colirrsE	1266	GCGAGAGCAAGCGGACCTCATAAAGTGCGTTCGTAGTCCGGATTGGAGTCTGCAACTCGACTC
Cam.jejun5	1245	GCGAGGTGGAG-CAAAATCTATAAAATATGTCCAGTTCGGATTGTTCTCTGCAACTCGAGAG
Stp.aureus	1276	GCGAGGTCAAGCAAATCCCATAAAGTTGTTCTCAGTTCGGATTGTAGTCTGCAACTCGACTA
E.colirrsE	1328	CATGAAGTCGGAATCGCTAGTAATCGTGGATCAGA-ATGCCACGGTGAATACGTTCCCGGGC
Cam.jejun5	1306	CATGAAGCCGGAATCGCTAGTAATCGTAGATCAGCCATGCTACGGTGAATACGTTCCCGGGT
Stp.aureus	1338	CATGAAGCTGGAATCGCTAGTAATCGTAGATCAGC-ATGCTACGGTGAATACGTTCCCGGGT
1743 (compl)		CGGTGAATACGTTCCCGGGC

FIG. 89E

E.colirrsE	1389	CTTG	TACACACCGCCCGTCACACCATGGGAGTGGGTTGCAAAAGAGTAGGTAACCT
Cam.jejun5	1368	CTTG	TA CT CACCGCCCGTCACACCATGGGAGTTGATTTCACTCGAAGCCGGAATACT--A-A
Stp.aureus	1399	ATTG	TACACACCGCCCGTCACACACGAGAGTTTGTAAACACCCGAAGCCGGTGGAGTAACCT
1743(compl)		CTTG	TAC
E.colirrsE	1451	TCG	GGAGGGCGCTTACCACCTTTGTGATTCATGACTGGGGTGAAGTCGTAACAAGGTAACCG
Cam.jejun5	1427	AC--T	AGTTACCGTCCACAGTGGAATCAGCGACTGGGGTGAAGTCGTAACAAGGTAACCG
Stp.aureus	1461	TTTAGGAGCTAGCCGTCGAAGGTGGGACAAATGATTGGGGTGAAGTCGTAACAAGGTAAGCCG	
E.colirrsE	1512	TAGGGGAACCTGCGGTTGGATCACCTCCTTA---	
Cam.jejun5	1485	TAGGAGAACCTGCGGTTGGATCACCTCCT-----	
Stp.aureus	1523	TATCGGAAGGTGCGGCTGGATCACCTCCTTTCT-	

FIG. 89F

1389 1368 1399 1451 1427 1461 1512 1485 1523

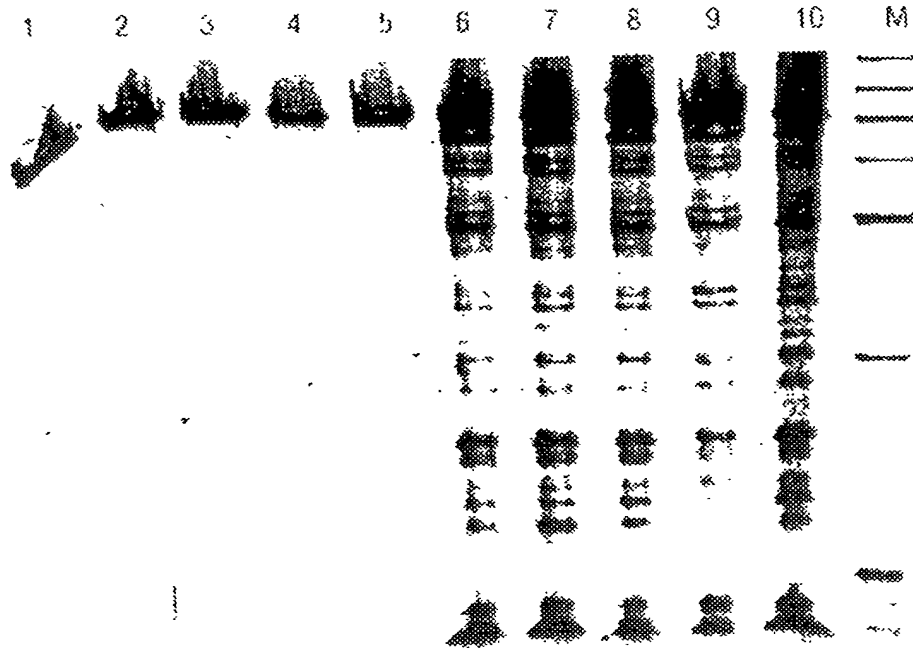


FIG. 91A

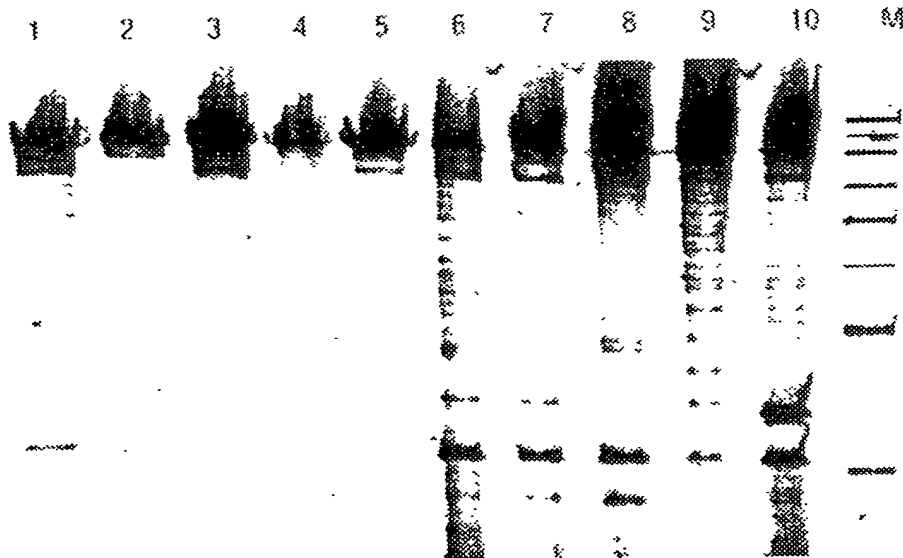


FIG. 91B



FIG. 92

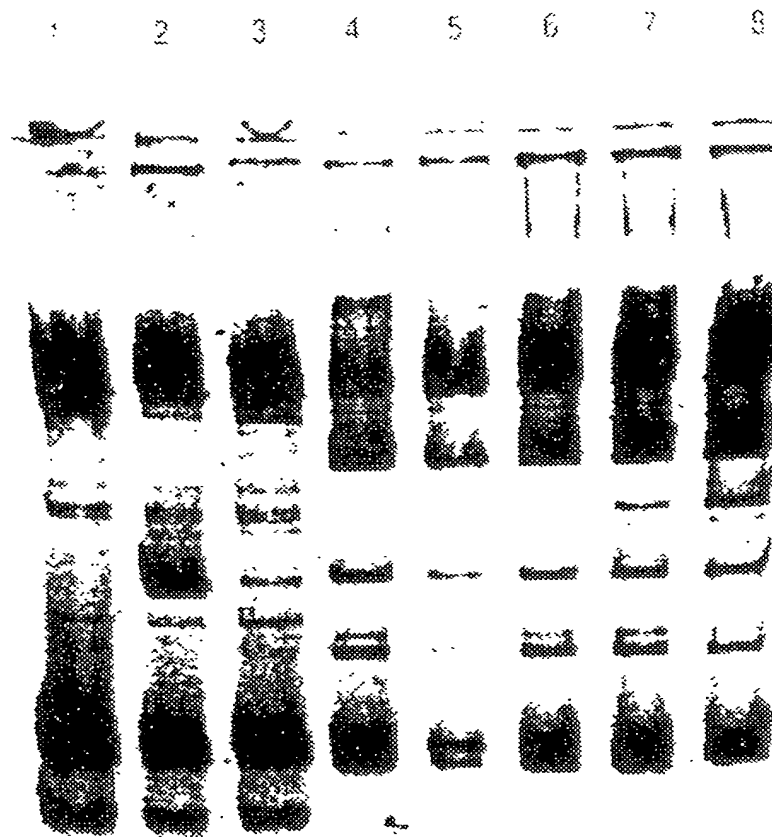


FIG. 93

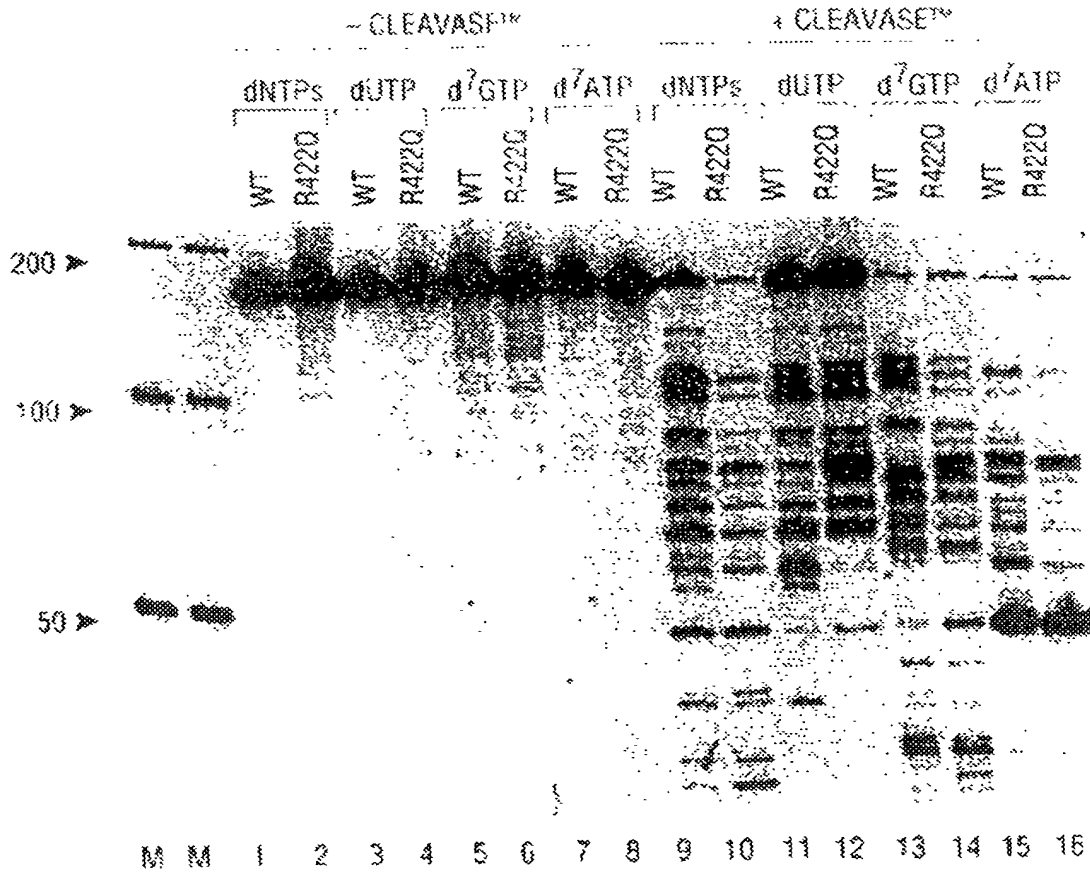


FIG. 94